Access DB# 8/357

SEARCH REQUEST FORM

Scientific and Technical Information Center

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Requester's Full Name:		Examiner # :	Date:
. at Omt.	none number 30	Serial Number	
Mail Box and Bldg/Room L	ocation:	Results Format Preferred (ci	rcle): PAPER DISK E-MAI
If more than one search is	submitted, please p	orioritize searches in order o	f need.
Please provide a detailed statemer Include the elected species or stru	nt of the search topic, and d ctures, keywords, synonym ry terms that may have a sp	describe as specifically as possible the ns, acronyms, and registry numbers; pecial meaning. Give examples or re-	e subject matter to be searched.
Title of Invention:			
Inventors (please provide full na	mes):		
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Earliest Priority Filing Date:			
For Sequence Searches Only Plea appropriate serial number.	se include all pertinent infor	mation (parent, child, divisional, or issu	ed patent numbers) along with the
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TAFF USE ONLY	Type of Search	*******	*****
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Other

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Maximum Match 100%
Listing first 45 summaries
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Maximum DB
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486	330	1157	1004	222	1358	1314	857	459	1553	1100	1643	1151	612	761	603
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ALIGNMENTS

Db 2	Qy 2	0y 1 0b 1	Db 1	Qy 1	Db	Qy	Db	Qy	Query Best Match	A; MOIEC A; Resid A; Cross C; Keywo	submitt A; Refer A; Acces	A;Residues A;Cross-re R:Wang, X.	A;Statu A;Molec	A; Title A; Refer A; Acces	R;Wang, EMBO J.	cystein C;Speci C;Date:	RESULT S64710
230 LEFMHILTRVNRKVATEFESFSLDSTFHAKKQIPCIVSMLTKELYF 275	RHFESQSDDF	196 QADSGPINDTDANPRYKIPVEADFLFAYSTVPGYYSWRSPGRGSWFVQALCSILEEHGKE 255	113 SFVCVILSHGDEGVIFGTDGPIDLKKLTSYFRGDRCRSLIGKPKLFIIQACRGTELDCGI 172	136 CFACILLSHGEENVIYGKDGVTPIKDLTAHFRGDRCKTLLEKPKLFFIQACRGTELDDAI 195	53 KNFHKSTGMTPRSGTDVDAAKLRETFMNLKYEVRNKNDLTREEIVELMKNASKEDHSKRS 112	76 KNFDKVTGMGVRNGTDKDAEALFKCFRSLGFDVIVYNDCSCAKMQDLLKKASEEDHTNAA 135	4 NETSYDSKSIKNFEYKTIHGSKSMDSGIYLDSSYKMDYPEMGYCIIINN 52	FSKKKKNVTMRSIKTTRDRVPTYQYI	Query Match 46.6%; Score 751; DB 2; Length 277; Best Local Similarity 52.4%; Pred. No. 2.5e-57; Matches 150; Conservative 46; Mismatches 74; Indels 16; Gaps 3;	A; MOLECULE Type: MRNA A; ACSIDER: 1-79, 'A', 81-146,'Y', 148-277 <waw>A; Cross-references: EMBL:U27463; NID:g12444443; PIDN:AAB01511.1; PID:g1244444 C; Keywords: apoptosis; cysteine proteinase; hydrolase</waw>	submitted to the EMBL Data Library, May 1995 A;Reference number: S72395 A;Accession: S72395	A;Residues: 1-277 <wan> A;Cross-references: EMBL:U27463 R:Wang. X</wan>	A;Status: nucleic acid sequence not shown A;Molecule type: mRNA	A;Pitle: Cleavage of sterol regulatory element binding proteins (SREBPs) by CPP32 dur A;Reference number: S64710; MUID:96183185; PMID:8605870 A;Accession: S64710	EMBO J. 15, 1012-1020, 1996	<pre>Cysteine proteinase (EC 3.4.22) CPP32 - Chinese namster C;Species: Cricetulus griscus (Chinese hamster) C;Date: 14-Feb-1997 #sequence_revision 13-Mar-1997 #text_change 05-Nov-1999 C;Date: 16-1997 #sequence_revision 13-Mar-1997 #text_change 05-Nov-1999</pre>	

coagulation factor

RESULT 2 A55315

cysteine proteinase (EC 3.4.22.-) CPP32 precursor - human

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R; Mukasa, T.; Urase, K.; Momoi, M.Y.; Kimura, I.; Momoi, T. Biochem. Biophys. Res. Commun. 231, 770-774, 1997
A; Title: Specific expression of CPP32 in sensory neurons of A; Reference number: JC5410; MUID:97224429; PMID:9070890
A; Accession: JC5410
A; Status: nucleic acid sequence not shown
                                                                                                                                                                                                                                  CPP32 protein - mouse
C;Species: Mus musculus (house mouse)
C;Date: 10-Jun-1997 #sequence_revision 18-Jul-1997 #text_change
C;Accession: JC5410
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JC5410
A; Experimental source:
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                              A; Cross-references: DDBJ: D86352
                                                 A; Molecule type: mRNA
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A;Molecule type: mRNA
A;Molecule type: mRNA
A;Residues: 1-189, 'E',191-277 <RES>
A;Cross-references: EMBL:U26943; NID:g857568; PIDN:AAA74929.1;
C;Keywords: apoptosis; cysteine proteinase; hydrolase; lymphocy
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C;Species: Homo sapiens (man)
C;Date: 06-Feb-1995 #sequence_revision 06-Feb-1995 #text_change 01-Dec-2000
C;Accession: A5515; S5889; I39005
R;Fernandes-Alnemri, T; Litwack, G; Alnemri, E.S.
J. Biol. Chem. 269, 30761-30764, 1994
A;Title: CPP32, a novel human apoptotic protein with homology to Caenorhabd.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 A; Residues: 29-46; 176-189, 'E', 191-193 < NIC>
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R;Nicholson, D.W.; Ali, A.; Thornberry, N.A.; Vaillancourt, J.P.; Ding,
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A; Status: preliminary
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A; Residues: 1-277 <FER>
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       embryo
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      PID: 9857569
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RESULT A49429

Interleukin 1 beta-converting enzyme homolog CED-3 - Caenorhal C;Species: Caenorhabditis elegans
C;Date: 07-Apr-1994 #sequence_revision 18-Nov-1994 #text_chang
C;Accession: A49429; T37312

Ledoux,

s.;

Ellis, H.M.; Horvitz,

H.R

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                                                                                                                                                                                                                                                                                                                             C; Keywords: cysteine proteinase;
                                                                                                                                                                                                                                                                                                                                                             A; Molecule type: mRNA
A; Residues: 1-212 < RES>
                                                                                                                                                                                                                                                                                                                                                                                                             nulosa cells of the ovarian follicle.
A;Reference number: I53300; MUID:96042508; PMID:7588240
A;Accession: I67437
                                                                                                                                                                                                                                                                                                                                                                                                                                                                       R;Flaws, J.A.; Kugu, K.; Trbovich, A.M.; DeSanti, A.;
Endocrinology 136, 5042-5053, 1995
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             C;Accession: I67437
R;Flaws, J.A.; Kugu,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        cysteine proteinase (EC 3.4.22.-) p32 - rat (fragment)
C:Species: Rattus norvegicus (Norway rat)
C:Date: 26-Jul-1996 #sequence_revision 26-Jul-1996 #te
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            RESULT
167437
                                                                                                                                                                                                                                                                                                                                         A; Cross-references: EMBL: U34685; NID: g1004370; PIDN: AAC52261.1; PID: g1004371
                                                                                                                                                                                                                                                                                                                                                                                              A; Status: preliminary; translated from
                                                                                                                                                                                                                                                                                                                                                                                                                                                                A; Title:
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Best Local :
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                                                                                                                                 83
                                                                                                                                                                                                                            60 YNMNFEKLGKCIIINNKNFDKVTGMGVRNGTDKDAEALFKCFRSLGFDVIVYNDCSCAKM 119
                                                                                                                                                                                                                                                                             Local
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                                                                              LFFIQACRGTELDDAIQADSGPINDTDANPRYKIPVEADFLFAYSTVPGYYSWRSPGRGS
 WFIQSLCAMLKLYAHKLEFMHILTRVN
                                                                                                                             MELMDSVSKEDHSKRSSFVCVILSHGDEGVIFGTNGPVDLKKLTSFFRGDYCRSLTGKPK
                                                                                                                                                             QDLLKKASEEDHTNAACFACILLSHGEENVIYGKDGVTPIKDLTAHFRGDRCKTLLEKPK 179
                                                                                                                                                                                            YKMDYPEMGLCIIINNKNFHKSTGMSARNGTDVDAANLRETFMALKYEVRNKNDLTREEI
                                WFVQALCSILEEHGKELEIMQILTRVN
                                                                LFIIQACRGTELDSGIETDSGADDDVACQ ---
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         QADSGPINDTDANPR-YKIPVEADFLFAYSTVPGYYSWRSPGRGSWFVQALCSILEEHGK
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         CFACILLSHGEENVIYGKDGVTPIKDLTAHFRGDRCKTLLEKPKLFFIQACRGTELDDAI
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           SFVCVILSHGDEGVIFGTNGPVDLKKLTSFFRGDYCRSLTGKPKLFIIQACRGTELDCGI
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            NKTSVDSKSINNFGVKTIHGSKSVDSGIYLDS------SYKMDYPEMGICIIITN
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                                                                                                                                                                                                                                                                             Similarity
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                                                                                                                                                                                                                                                                             36.0%;
52.7%;
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50.2%; Pred. No.
                                                                                                                                                                                                                                                            37;
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                                                                                                                                                                                                                                                                                                                             hydrolase
                                                                                                                                                                                                                                                                             Pred. No. 9.8e-43;
                                                                                                                                                                                                                                                                                           Score 580.5;
                                                                                                                                                                                                                                                              Mismatches
211
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                                                                KKPVEADFLYAYSSAPGYYSWRNSRGGS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          7.8e-53;
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                                                                                                                                                                                                                                                              58;
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Caspase-9 long chain - mouse
C:Species: Mus musculus (house mouse)
C:Species: Aus musculus (house mouse)
C:Date: 23-Mar-2001 #sequence_revision 23-Mar-2001 #text_change 23-Mar-2001
C:Accession: JC7123
R:Fujita, E:; Jinbo, A.; Matuzaki, H.; Konishi, H.; Kikkawa, U.; Momoi, T.
Biochem. Biophys. Res. Commun. 264, 550-555, 1999
A:Title: Akt phosphorylation site found in human caspase-9 is absent in mous A; Reference number: JC7123; MUID:20001956; PMID:10529400
A; Accession: JC7123
A; Status: preliminary
A; Status: preliminary
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         A;Residues: 1-503 <YUA>
A;Residues: 1-503 <YUA>
A;Cross:references: GB:L29052; NID:g6503232; PIDN:AAA27982.2; PID:g6503233
A:Note: sequence extracted from NCBI backbone (NCBIN:139825, NCBIP:139826)
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                                                                                                                                                                                                                                     A;Molecule type: mRNĀ
A;Residues: 1-454 <FUJ>
A;Cross-references: DDBJ:AB019600; NID:g6440941; PID:g6440942
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JC7123
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A;Gene: ced-3
A;Introns: 45/3;
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A; Residues: 1-417,'R',419-503 < YU2>
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A;Molecule type: DNA
A;Residues: 1-503 <YU
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Best Local Similarity
                                                                                                                                                                        Query Match
Best Local Similarity
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  187 GC-SSLGYSSSRNRSFSKA----SGPTQYIFHEEDMNFVDAPTISRVFDEKTMYR---NF 238
                                                               191 YTLDSDPCGHCLIINNVNFCRSSGLGTRTGSNIDRDKLEHRFRWLRFMVEVKNDLTAKKM 250
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                                                                                                          60 YNMNFEKLGKCIIINNKNFDKVTGMGVRNGTDKDAEALFKCFRSLGFDVIVYNDCSCAKM 119
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QDLLKKASEEDHTNAACFACILLSHGEE-----NVIYGKDGVT-PIKDLTAHFRGDRC 171
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ARHFESQSDDPHFHEKKQIPCVVSMLTKELYF 301
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             WRKKPSQADILIAYATTAQYVSWRNSARGSWFIQAVCEVFSTHAKDMDVVELLTEVNKKV 465
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      --KIPVEADFLFAYSTVPGYYSWRSPGRGSWFVQALCSILEEHGKELEIMQILTRVNDRV
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    KIVFVQACRGERRDNGF-----PVLDSVDGVPAFLRRGWDNRDGPLFNFLGCVRPQVQQV 405
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            KLFFIQACRGTELDDAIQADSGPINDT-DANPRY--
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     RDFAKHESHGDSAIL--VILSHGEENVIIGVDDIPISTHEIYDLLNAANAPR---LANKP 350
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  EK-LGKCIIINNKNFDKVTGMGVRNGTDKDAEALFKCFRSLGFDVIVYNDCSCAKMQDLL 123
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             GCIEEQGVEDSANEDSVDAKPDRSSFVPSLFSKKKKN-VTMRSIKTTRDRVPTYQYNMNF
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                                                                                                                                                        90;
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                                                                                                                                                     43;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Score 377; DB 2; Pred. No. 1.1e-24;
                                                                                                                                                                          Score 371.5; DB Pred. No. 3e-24;
                                                                                                                                                     Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         494
                                                                                                                                                                                              DB 2;
                                                                                                                                                     96;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Length
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Indels
                                                                                                                                                                                              Length
                                                                                                                                                   Indels
                                                                                                                                                                                                                                                                                                                                                                           absent in mouse
                                                                                                                                                   45;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          60;
                                                                                                                                                   Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      269
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RESULT
G02635
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                                                                                                                                                                                                                                                                                                        QΥ
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R;Duan, H.; Orth, K.; Chinnaiyan, A.M.; Poirier, G.G.; submitted to the EMBL Data Library, April 1996
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Ş
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                                                                                                                                                                                                                                                                                                                                                                                                                              A; Molecule type: mRNA
A; Residues: 1-416 < DUA>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                A; Reference number: H01513
A; Accession: G02635
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   C; Species: Homo sapiens (man)
C; Date: 21-Dec-1996 #sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           B
                                                                                                                                                                                                                                                                                                                                                                                                              A;Cross-references: EMBL:U56390; NID:g1336026; PIDN:AAC50640.1; PID:g1336027
                                                                                                                                                                                                                                                                                                                                                                                                                                                                A; Status: preliminary; translated from GB/EMBL/DDBJ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ICE-LAP6 -
                                                                                                                                                                                                                                                                                                                                           Matches
                                                                                                                                                                                                                                                                          153
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           431
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            371
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                               271
                                                                 333
                                                                                                  213
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  251
                                                                                                                                                                                                       213 VLALLELARQDHGALDCCVVVILSHGCQASHLQFPGAVYGTDGCPVSVEKIVNIFNGTSC
                                                                                                                                                                                                                                                                                                          60 YMMNFEKLGKCIIINNKNFDKVTGMGVRNGTDKDAEALFKCFRSLGFDVIVYNDCSCAKM 119
                                                                                                                                                                                                                                                                                                                                                             Local
                                                                                                                                                                                                                                                                          YILSMEPCGHCLIINNVNFCRESGLRTRTGSNIDCEKLRRRFSSLHFMVEVKGDLTAKKM
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               KTLLEKPKLFFIQACRGTELDD----AIQADSGPINDTDANPR--
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  YTALMEMAHRNHRALDCFYYYILSHGCQASHLQFPGAYYGTDGCSYSIEKIYNIFNGSGC
                                                                                  --IPVEADFLFAYSTVPGYYSWRSPGRGSWFVQALCSILEEHGKELEIMQILTRVNDRVA 270
                                                                                                                                                       QDLLKKASEEDHTNAACFACILLSHGEE-----NVIYGKDGV-TPIKDLTAHFRGDRC 171
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           RHFESQSDDPHFHEK----KQIPCVVSMLTKELYF
                              RHFESQSDDPHFHEK---KQIPCVVSMLTKELYF
                                                                 SSLPTPSDIFVSYSTFPGFVSWRDPKSGSWYVETLDDIFEQWAHSEDLQSLLLRVANAVS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            SSLPTPSDILVSYSTFPGFVSWRDKKSGSWYIETLDGILFQWARSEDLQSLLLRVANAVS 430
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            YKIPVEADFLFAYSTVPGYYSWRSPGRGSWFVQALCSILEEHGKELEIMQILTRVNDRVA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             PSLGGKPKLFFIQACGGEQKDHGFEVACTSSQGRTLDSDSEPDATPFQEGPRPLDQLDAV 370
                                                                                                                                    PSLGGKPKLFFIQACGGEQKDHGFEVASTSPEDESPGSNPEPDATPFQEGLRTFDQLDAI
                                                                                                                                                                                                                                                                                                                                           88;
                                                                                                                                                                                                                                                                                                                                                             Similarity
                                                                                                                                                                                                                                                                                                                                           Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    #sequence_revision 06-Jun-1997 #text_change 05-Nov-1999
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         EKGTYKQIPGCFNFLRKKLFF
 VKGIYKQMPGCFNFLRKKLFF
                                                                                                                                                                                                                                                                                                                                                         22.0%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Library, April
                                                                                                                                                                                                                                                                                                                                          ; Score 354.5; DB 2; pred. No. 7.9e-23; 41; Mismatches 100;
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                               301
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T20038

RESULT 8

15-Oct-1999

R;Burton, J. submitted to the EMBL Data Library, October 1996 a-Reference number: Z19214

A; Reference number: A; Accession: T20038

A; Status: preliminary; translated from GB/EMBL/DDBJ

A; Molecule type: DNA A; Residues: 1-495 <WIL> A; Cross-references: EMB

A; Experimental source: EMBL: Z81049; clone C48D1 PIDN:CAB02848.1; GSPDB:GN00022; CESP:C48D1.2

C;Genetics:
A;Gene: CESP:C48D1.2

position:

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apoptosis regulator ICH-1, stimulatory form L - human C:Species: Homo sapiens (man) C:Date: 28-Apr-1995 #sequence_revision 28-Apr-1995 #text_change 17-Mar-1999 C:Accession: A54821 R:Wang, L.; Miura, M.; Bergeron, L.; Zhu, H.; Yuan, J. Cell 78, 739-750, 1994 A:Title: ICh-1, an Ice/ced-3-related gene, encodes both positive and negative A:Reference number: A54821; MUID:94373811; PMID:8087842 A:Accession: A54821
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A; Residues: 1-435 <WAN>
                                                                                                                                                                                                                                                                                                                                                                                                                                                           A; Status: preliminary
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                                                                                                                                                                                                                                                                                                                               Matches
                                                                                                                                                                                                                                                                                                                                                              Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Matches
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Best Local
                                                                                                                                                                                                                              120
 413
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                                286
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                                                                                                                                                                                                                                                                                           60 YNMNFEKLGKCIIINNKNFDKVTGMGVRNGTDKDAEALFKCFRSLGFDVIVYNDCSCAKM 119
                                                                                                                                                                                                                                                                                                                                              Local
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             22
                                                                                                                                                                                                                                                         YRLQSRPRGLALVLSNVHFTGEKELEFRSGGDVDHSTLVTLFKLLGYDVHVLCDQTAQEM 234
                                                                                                                                                                                                                           QDLLKKASEEDHTNAACFACI--LLSHGEENVIYGKDG-VTPIKDLTAHFRGDRCKTLLE 176
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       RVFDEKTMYRNFSSPRGMCLIINNEHFEQ---MPTRNGTKADKDNLTNLFRCMGYTVICK
 KEMSEYCSTLCRHLY
                                                         LKGTAAMRNTKRGSWYIEALAQVFSERACDMHVADMLVKVN-ALIKDREGYAPGTEFHRC
                                                                                           VPGYYSWRSPGRGSWFVQALCSILEEHGKELEIMQILTRVNDRVARHFESQSDDPHFHEK 285
                                                                                                                                                          KPKLFFIQACRGTELDDAIQADSGP-----INDTDAN----PRYKIPVEADFLFAYST
                                                                                                                                                                                           QEKLQNFAQLP-AHRVTDSCIVALLSHGVEGAIYGVDGKLLQLQEVFQLFDNANCPSLQN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            VVELLTEVNKKVA 465
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         NAPR---LANKPKIVFVQACRGERRDNGF--
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      VNAFPSQPSSANSSFT----GCSSLGYSSSRNRSFSKASGPTQYIFHEEDMNFVDAPTIS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      VDAKPDRSSFVPSLFSKKKKNVTMRSIKTTRDRV-----PT----YQYNMNF--
                              KQIPCVVSMLTKELY
                                                                                                                            KPKMFFIQACRGDETDRGVDQQDGKNHAGSPGCEESDAGKEKLPKMRLPTRSDMICGYAC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         FLGCVRPQVQQVWRKKPSQADILIAYATTAQYVSWRNSARGSWFIQAVCEVFSTHAKDMD
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      RGDRCKTLLEKPKLFFIQACRGTELDDAIQADSGPINDT-DANPRY--------
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        DNLTGRGMLLTIRDFAKHESHGDSAIL--VILSHGEENVIIGVDDIPISTHEIYDLLNAA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         NDCSCAKMQDLLKK-ASEEDHTNAACFACILLSHGEENVIYGKDGVT----PIKDLTAHF
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ----EKL------GKCIIINNKNFDKVTGMGVRNGTDKDAEALFKCFRSLGFDVIVY 111
                                                                                                                                                                                                                                                                                                                             75; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              97;
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                                                                                                                                                                                                                                                                                                                            Conservative
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                                                                                                                                                                                                                                                                                                                                                                                           splicing;
                              300
                                                                                                                                                                                                                                                                                                                                             19.7%;
427
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     21.7%; Score 349.5; DB 2;
31.0%; Pred. No. 2.7e-22;
40. Mismatches 87;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       288/3; 360/1; 402/3; 466/1
                                                                                                                                                                                                                                                                                                                            52;
                                                                                                                                                                                                                                                                                                                                         Score 317; DB 2;
Pred. No. 1.5e-19;
                                                                                                                                                                                                                                                                                                                                                                                           apoptosis
                                                                                                                                                                                                                                                                                                                            Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                        PID:g537292
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        PVLDSVDGVPAFLRRGWDNRDGPLFN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       DB 2;
                                                                                                                                                                                                                                                                                                                            112;
                                                                                                                                                                                                                                                                                                                                                         Length 435;
                                                                                                                                                                                                                                                                                                                            Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Length 495;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Indels
                                                                                                                                                                                                                                                                                                                            16;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          81;
                                                                                                                                                                                                                                                                                                                        Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         negative regulator
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                                                                                                                                                                                           293
                                                                                                                          353
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Gene 202, 127-132, 1997
A.Title: Cloning and expression of the cDNA encoding rat A;Reference number: JC6507; MUID:98087427; PMID:9427555
A;Accession: JC6507
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C:Species: Rattus norvegicus (Norway rat)
C:Date: 16-Jul-1999 #sequence_revision 16
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              RESULT
JC6507
                                                                                                                                                                                                                                                                                                                                                                                                                            A; Cross-references: GB: U77933; NID: g2769705; PIDN: AAB96379.1; PID: g2769706
                                                                                                                                                                                                                                                                                                                                                                                                                                              A; Molecule type: mRNA
A; Residues: 1-452 <SAT>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    R; Sato, N.; Milligan, C.E.; Uchiyama,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      C; Accession: JC6507
                                                                                                                                                                                                                                                                                                                                                                          Query Match
Best Local
                                                                                                                                                                                                                                                                                                                                                           Matches
426
                                                                                                       222
                                                                                                                                                          116 CAKMQDLLKKASEEDHTNAACFACI--LLSHGEENVIYGKDG-VTPIKDLTAHFRGDRCK 172
                                                                                                                                                                                                                                                                                188 YQLAYRLQSQPRGLALVMSNVHFTGEKDLEFRSGGDVDHTTLVTLFKLLGYNVHVLYDQT
                                                                                                                                    307 SLQNKPKMFFIQACRGDETDRGVDQQDGKNHAQSPGCEESDAGKEELMKMRLPTRSDMIC 366
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                10
FHRCKEMSEYCSTLCQQLY
                                 FHEKKQIPCVVSMLTKELY 300
                                                                                                 AYSTVPGYYSWRSPGRGSWFVQALCSILEEHGKELEIMQILTRVNDRVARHFESQSDDPH
                                                                                                                                                                                                            AQEMQEKLQNFAQLP-AHRVTDSCIVALLSHGVEGGIYGVDGKLLQLQEVFRLFDNANCP
                                                                    GYACLKGNAAMRNTKRGSWYIEALTQVFSERACDMHVADMLVKVN-ALIKEREGYAPGTE 425
                                                                                                                                                                                                                                                                                                                   YQ--YNMNFEKLGKCIIINNKNFDKVTGMGVRNGTDKDAEALFKCFRSLGFDVIVYNDCS
                                                                                                                                                                                                                                                                                                                                                       76;
                                                                                                                                                                                                                                                                                                                                                                        Similarity
                                                                                                                                                                                                                                                                                                                                                       Conservative
                                                                                                                                                                                                                                                                                                                                                                        18.9%;
29.3%;
444
                                                                                                                                                                                                                                                                                                                                                       55;
                                                                                                                                                                                                                                                                                                                                                                        Score 305; DB 2;
Pred. No. 1.7e-18;
                                                                                                                                                                                                                                                                                                                                                       Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ۲.;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Oppenheim,
                                                                                                                                                                                                                                                                                                                                                       110;
                                                                                                                                                                                                                                                                                                                                                                                       Length 452
                                                                                                                                                                                                                                                                                                                                                       Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   caspase-2
                                                                                                                                                                                                                                                                                                                                                       18;
                                                                                                                                                                                                                                                                                                                                                      Gaps
                                                                                                                                                                         221
                                                                                                                                                                                                            306
                                                                                                                                                                                                                                                                                247
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RESULT T43638

C;Species: Caenorhabditis elegans C;Date: 21-Jan-2000 #sequence_revision C;Accession: T43638; T43639 N; Contains: caspase 2B caspase-related proteinase 2A (EC 3.4.22.-) -21-Jan-2000 Caenorhabditis #text_change elegans 21-Jul-2000

J. Biol. Chem. 273, 35109-35117, 1998
A; Title: Identification of multiple Caenorhabditis elegans
A; Reference number: Z22587; MUID:99074291; PMID:9857046 A;Status: preliminary; translated from GB/EMBL/DDBJ A; Accession: T43638 caspases

and

their

potenti

R;Shaham,

A; Cross-references: A; Accession: T43639 A; Molecule type: mRNA A; Residues: 1-826 <SHA> Status: preliminary; translated EMBL: AF088288;

A; Molecule type: mRNA A; Residues: 564-826 < A; Cross-references: Genetics: EMBL: AF088289; <SH2> NID:g4063375; PIDN: AAC98296.1; PID:g4063376

from

GB/EMBL/DDBJ

NID:g4063373; PIDN:AAC98295.1;

PID:g4063374

A;Gene: csp-2 A;Map position: 4 C;Keywords: cysteine proteinase; hydrolase

Matches Query Match Best Local Similarity Conservative 18.9%; 53; Score 305; DB 2; Pred. No. 3.6e-18; 3; Mismatches 96; Length 826 Indels 36; Gaps

8

δÃ 57 TYQYNMNFEKLGKCIIINNKNFDKVTGMGVRNGTDKDAEALFKCFRSLGFDVIVYNDCSC 116 | :| | :| | :| | :: | :: | ::

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δÃ
                                                                                                                                                                                                                                                                                                                                                                                                                                                   C; Keywords: cysteine proteinase;
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A; Residues: 269-536 <
A; Cross-references: E
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J. Biol. C
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        J. Biol. Chem. 273, 35109-35117, 1998
A;Title: Identification of multiple Caenorhabditis elegans
A;Reference number: 222587; MUID:99074291; PMID:9857046
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RESULT
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            caspase-related proteinase 1A
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Best Local
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Function:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Molecule type: mRNA
Residues: 1-536 <SHA>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Status: preliminary; translated from GB/EMBL/DDBJ
                                                                                                                                                                                                                                                                                                                                                                                      Matches
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                                                   513
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                                                  NVVL---
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                                                                                                                                                                                                               TLLEKPKLFFIQACRGTELDDAIQADSGPINDTDANPRYKI--
                                                                                                                                                                                                                                                SMLEAIKEFAEMAHTDS--IILFLLSHGDGAGSVFGIDDMPVNVMEVSTYLAYH-----Q 392
                                                                                                                                                                                                                                                                                KMQDLLKKASEEDHTNAACFACILLSHGE-ENVIYGKD----GVTPIKDLTAHFRGDRCK 172
                                                                                                                                                                                                                                                                                                                 YCYEMNSNPRGTVLILSNENF---KNMERRVGTKQDEVNLTKLFQKLQYTVICKRNLEAE 339
                                                                                                                                                                                                                                                                                                                                      YQYNMNFEKLGKCIIINNKNFDKVTGMGVRNGTDKDAEALFKCFRSLGFDVIVYNDCSCA 117
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ---SLAKKPKWLMCVCCRGDRIDRAVRCDGFIDNFFDRFPKFFQFMKSKFPSHQTSSSQA
                                                                                 DPHFHEKKQIPCVVSMLTKELYFSQ 303
                                                                                                                VIISFSTTDGFTSYRDEEAGTWYIKSMCKVFNKHSKTMHLLDILTETGRNVVTKYENVQG 512
                                                                                                                                               FLFAYSTVPGYYSWRSPGRGSWFVQALCSILEEHGKELEIMQILTRVNDRVARHFESQSD
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 TRKYRNNRSSKCRAIIINNYYF---CGMEKRIGSDKDKKKLSKLFERLGYQSTSYDNLKS
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                                                   KQAPEILSRLTKQWHFSR 534
                                                                                                                                                                                                                                                                                                                                                                                      Conservative
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(B)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                        hydrolase
                                                                                                                                                                                                                                                                                                                                                                                                    Score 284; DB 2;
Pred. No. 1.4e-16;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                      cascades
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                                                                                                                                                                                                                                                                                                                                                                                   32;
                                                                                                                                                                                                                  -PVEAD
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                                                                                                                                                                                                                                                                                                                                                                                                           hypothetical protein Y48E1B.13 - Caenorhabditis elegans C;Species: Caenorhabditis elegans C;Decies: Caenorhabditis elegans C;Date: 15-Oct.1999 #sequence_revision 15-Oct.1999 #text_change 15-Oct.1999 C;Accession: T27021
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       T2702
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A;Title: Caspase-14: Analysis of gene structure and mRNA
A;Reference number: JC7517; MUID:20517231; PMID:11062009
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       C;Species: Homo sapiens (man)
C;Date: 30-Jun-2001 #sequence_revision 30-Jun-2001 #text_change
C;Accession: JC/517
R;Eckhart, L.; Ban, J.; Fischer, H.; Tschachler, E.
                                                                                                                                                       A; Introns:
                                                                                                                                                                                           A; Gene: CESP:Y48E1B.13
                                                                                                                                                                                                                                 A;Cross-references: EMBL:Z93393; PIDN:CAB07698.1; A;Experimental source: clone Y48E1B
                                                                                                                                                                                                                                                                     A; Molecule type: DNA
A; Residues: 1-642 <WIL>
                                                                                                                                                                                                                                                                                                                                               A; Reference number: Z20299
                                                                                                                                                                                                                                                                                                                                                                                       R; McMurray, A.
                                                                                                                                                                                                                                                                                                                                                                                                         C; Accession:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        A; Map position: 19p13.1
A; Introns: 9/3; 59/3; 135/1; 174/1;
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C;Comment: This enzyme accumulates
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         caspase-14/a - human
                                                                                                                                                                         A; Map position:
                                                                                                                                                                                                                                                                                                         A; Status: preliminary;
                                                                                                                                                                                                                                                                                                                             A; Accession:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           RESULT 14
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-- rocal Similarity
                                                                                             Query Match
Best Local Similarity
                                                                                                                                                                                                               Genetics:
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YCYEMNSNPRGTVLILSNENF --- KNMERRVGTKQDEVNLTKLFQKLQYTVICKRNLEAE 417
                                     YOYNMNFEKLGKCIIINNKNFDKVTGMGVRNGTDKDAEALFKCFRSLGFDVIVYNDCSCA 117
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     LRKRLY 240
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  PGRGSWFVQALCSILEEHGKELEIMQILTRVNDRVARHFESQSDDPHFHEKKQIPCVVSM 294
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          RAKPKVYIIQACRGEQRDPGETVGGDEIVMVIKDSPQTIPTYTDALHVYSTVEGYIAYRH
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            LEKPKLFFIQACRGTELDDAIQADSGPINDTDANPRYKIPVEADFLFAYSTVPGYYSWRS 234
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              KYDMSGARLALILCVTK----
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        MQDLLKK----ASEEDHTNAACFACILLSHGEENVIYGKDG-VTPIKDLTAHFRGDRCKTL
                                                                                                                                                       79/3;
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                                                                                                                                                     122/3; 239/2; 286/3; 333/1;
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                                                                             Conservative
                                                                                                                                                                                                                                                                                                           translated from GB/EMBL/DDBJ
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28.0%;
                                                                                             15.5%;
                                                                                                                                                                                                                                                                                                                                                                   Library, March 1997
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            -----AREGSEEDLDALEHMFRQLRFESTMKRDPTAEQ
                                                                             41; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          46;
                                                                                           Score 250; DB 2;
Pred. No. 1.5e-13;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Score 255; DB 2;
Pred. No. 1.6e-14;
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                                                                                                                                                     417/3;
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                                                                                                                                                                                                                                                     GSPDB:GN00020;
                                                                                                                                                       487/1; 589/1;
                                                                                                             Length 642
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A;Map position: X
A;Introns: 30/3; 272/3; 393/3; 445/2
A;Note: EG:115C2.9
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           R:Salles, C.; Valenti, P.; Darlamitsou, A.; Henderson, N.; Campbell, L.; Glover, submitted to the EMBL Data Library, May 1999

A; Description: Sequencing the distal X chromosome of Drosophila melanogaster.
A; Reference number: Z17665
A; Accession: T1385
A; Status: preliminary; translated from GB/EMBL/DDBJ
A; Molecule type: DNA
A; Residues: 1-488 <CAT>
A; Residues: 1-488 <CAT>
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C:Species: Drosophila melanogaster
C:Date: 13-Aug-1999 #sequence_revision 13-Aug-1999 #text_change 17-Nov-2000
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Query Match
Best Local Similarity 25.5
Matches 81; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Cross-references: EMBL:AL031581; NID:e1320978; PID:e1331441; PIDN:CAA20893.1
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                                                                                   467
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                                                                                                                                                                                                                                                                                                                 304 VEAYDNVDHMGIIERIRSACDRSLVRDS-LVVFILSHGFEEAVYASNSIAMKITDIEDLL
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                               224 STVPGYYSWRSPGRGSWFVQALCSILEEHGKELEIMQILTRVNDRVARHFESQSDDPHFH 283
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                                                                                                                                                                                                                                    CSY----DTLYYKPKLLIIQACQEKLVHKKKPNELFRIDVTTVSPDQHI----DMLRAM
                                                                              DESMVPNVKSTFROHVYF
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Maximum Match 100%
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20000000000
       ICE1_DROME
ICE6_MOUSE
ICE6_HUMAN
ICE8_HUMAN
ICEA_HUMAN
CED3_CAEVU
CED3_CAEVU
CED3_CAEVL
ICE9_HUMAN
ICE2_RAT
I1BC_PIG
I1BC_HORSE
I1BC_RAT
                                                                                                    ICE2_HUMAN
ICEE_HOMSE
ICEE_HOMSE
ICEE_HOUSE
ICEE_KOUSE
ICEB_XENLA
ICEA_XENLA
ICEA_XENLA
ICEA_BOVIN
ICEC_CANPA
ICES_HUMAN
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Q9mzv7
P51878
P55215
Q9n211
Q9tv13
P43527
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P42573
P55211
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002002
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P55212
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P70677
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homo sapien
mus musculu
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caenorhabdi
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    drosophila drosophila
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    homo sapien
h caspase-8
                       sus scrofa
equus cabal
                                                                          homo sapien
rattus norv
                                                                                                                            bos taurus
canis famil
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felis silve
                                                                                                                                                                                                                                                                                                                                                          homo sapien
gallus gall
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mesocricetu
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rattus norv
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356	459	1100	603	282	484	480	419	377	402	373	404	
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CARA_THETN	FA9_MOUSE	RADI_YEAST	YB55_METJA	FA9_RAT	CFLA_MOUSE	CFLA_HUMAN	ICEC_MOUSE	ICE4_HUMAN	I1BC_MOUSE	ICEB_MOUSE	I1BC_HUMAN	
	P16294 mus musculu	P06777 saccharomyc	Q58555 methanococc	P16296 rattus norv	035732 m casp8 and	015519 h casp8 and	O08736 mus musculu .	P49662 homo sapien	P29452 mus musculu	mus	P29466 homo sapien	

ALIGNMENTS

rattus norv

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PRINTS; PR00376; ILIBCENZYME.
SMART; SM00115; CASC; 1.
PROSITE; PS01122; CASPASE_CYS; 1.
PROSITE; PS01121; CASPASE_HIS; 1.
PROSITE; PS50207; CASPASE_P10; 1.
PROSITE; PS50208; CASPASE_P20; 1.
                                                                                                                                                                                                                                                   EMBL;
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                                                                                                                                                                                                                                                                       This SWISS-PROT entry is copyright. It is produced through a collabora between the Swiss Institute of Bioinformatics and the EMBL outstatise the European Bioinformatics Institute. There are no restrictions on use by non-profit institutions as long as its content is in no modified and this statement is not removed. Usage by and for commer entities requires a license agreement (See http://www.isb-sib.ch/annot or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                    EMBL;
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        VARSPLIC
                                                              CHAIN
                                                                                                                                Pfam; PF00655; ICE_p10; 1. Pfam; PF00656; ICE_p20; 1.
                                                                                                                                                                                      MEROPS;
                        VARSPLIC
                                                      PROPEP
                                                                      PROPEP
                                                                             Hydrolase;
                                                                                                                                                InterPro; IPR002138; ICE_p10
InterPro; IPR001309; ICE_p20
                                                                                                                                                                InterPro; IPR002398; ICE.
                                                                                                                                                                      MIM; 601761;
                                                                                                                                                                               Genew;
                                                                                                                                                                                                             EMBL;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Fernandes-Alnemri
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            MEDLINE-96353838;
                                                                                                                                                                                                                                                                                                                                  SIMILARITY: BELONGS TO PEPTIDASE FAMILY C14.
CAUTION: WHAT WE CALL ALPHA' ISOFORM IS KNOWN IN REF.4
BUT AS BETA IS ALREADY DEFINED IN REF.3 WE HAVE CALLED
                                                                                                                                                                                                           J U39613; AAC50346.1; -...
U40281; AAC50352.1; -...
U37448; AAC50303.1; -...
U37449; AAC50304.1; -...
U67319; AAC51152.1; -...
U67320; AAC51153.1; -...
U67320; AAC51160.1; -...
                                                                                                                                                                                                                                                                                                                                                            VICE VERSA.
                                                                                                                                                                                               P42574;
                                                                                                                                                                                                      BC015799;
                                                                                                                                                                              HGNC: 1508;
                                                                                                                                                                                       C14.004;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   53838; PubMed=8755496;
Inemri T., Armstrong R.C.,
Illrich F., Fritz L.C., Trap
Alnemri E.S.;
                        24
199
207
144
186
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                                                                                                                                                                                                     AAH15799
                                                                            protease;
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                             198
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206
303
144
186
                                                                           Zymogen; Apoptosis; Alternative
                        Z
VIYGKDGVTPIKDLTAHFRGDRCKTLLEKPKLFFIQACRGT
ELDDGIQADSGPINDTDANPRYKIPVEADFLFAYSTVPGYY
                                             CASPASE-7
                                                            CASPASE-7 SUBUNIT
               M -> MDCVGWPPGRKWHLEKNTSCGGSSGICASYVTQM
(IN ISOFORM ALPHA').
                                     SPASE-7 SUBUNIT SIMILARITY.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         .C., Krebs J.,
Trapani J.A.,
                                              P11
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Srinivasula S.M.,
Tomaselli K.J.,
                                                                                                                                                                                                                                                                                                                                    AS BETA,
IT ALPHA'.
                                                                           splicing
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RESULT
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Best Local S
Matches 301
                                                                                                                                                      process.";
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CONFLICT
SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                         01-OCT-1996 (Rel. 34, Created)
01-OCT-1996 (Rel. 34, Last sequence update)
15-JUN-2002 (Rel. 41, Last annotation update)
Caspase-7 precursor (EC 3.4.22.-) (ICE-like apoptotic protease
(ICE-LAP3) (Apoptotic protease Mch-3) (SREBP cleavage activity
     -
                                                                                                                                   Proc.
                                                                                                                                                                                                                                   [1]
SEQUENCE FROM N.A., AND ....
SEQUENCE FROM N.A., AND ....
SEQUENCE FROM N.A., AND ....
                                                                                                                                                                                                                                                                                                                      CASP7 OR MCH3.
Mesocricetus auratus (Golden hamster).
Mesocricetus auratus (Golden hamster).
Craniata: Vertebrata; Euteleostomi;
Cricetinae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                      P55214;
01-OCT-1996 (Rel.
                                                                                                                                                                                                             Pai J.-T., Brown M.S., Goldstein J.L.;
                                                                                                                                                                                                                                MEDLINE-96224303; PubMed-8643593;
                                                                                                                                                                                                                                                                                               NCBI_TaxID=10036;
                                                                                                                                                                                                                                                                                                                 Mesocricetus
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BOND. OVEREXPRESSION F SIMILARITY).
- SUBUNIT: HETERODIMER C (BY SIMILARITY).
- SUBCELLULAR LOCATION:
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                                                                               REGULATORY ELEMENT BINDING PROTEINS CLEAVES POLY(ADP-RIBOSE) POLYMERASE
                                                                                                             Natl. Acad. Sci. U.S.A. FUNCTION: INVOLVED IN THE RESPONSIBLE FOR APOPTOSIS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         MADDQGCIEEQGVEDSANEDSVDAKPDRSSFVPSLFSKKKKNVTMRSIKTTRDRVPTYQY
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         FFIQACRGTELDDAIQADSGPINDTDANPRYKIPVEADFLFAYSTVPGYYSWRSPGRGSW
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FFIQACRGTELDDGIQADSGPINDTDANPRYKIPVEADFLFAYSTVPGYYSWRSPGRGSW
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        NMNFEKLGKCIIINNKNFDKVTGMGVRNGTDKDAEALFKCFRSLGFDVIVYNDCSCAKMQ
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                                                                 PROMOTES
 Cytoplasmic
                                                                                                                                                                               oning of a second apoptosis-related cysteine activates sterol regulatory element binding
                                A 20 kDa
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Pred.
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HFESQSSDDPHFHEKKQIPCVVSMLTKELLYFSQ -> MESCS
VTQAGVQRRDLGRLQPPPPRLAEGPSLMMASPPTRGPSMTQ
MLILDTRSQWKLTSSSPIPRFQAITRGGAQEEAPGLCKPSA
PSWRSTEKTWKSCRSSPG (IN ISOFORM BETA).
C->A: NO APOPTOTIC ACTIVITY.
                                                                          93:5437-5442(1996).
ACTIVATION CASCADE OF CASPASES
EXECUTION. CLEAVES AND ACTIVATES STEROL
G PROTEINS (SREBPS). PROTEOLYTICALLY
POLYMERASE (PARP) AT A 216-ASP-1-GLY-217
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-> A (IN REF. 1).
.CD373EE54A232CA4 CRC64;
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Best Local
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ICE7_MOUSE S
P97864; 008669;
01-NOV-1997 (Rel
01-NOV-1997 (Rel
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ACT_SITE
ACT_SITE
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PROSITE; PS01121; CASPASE_H1S; 1.
PROSITE; PS50207; CASPASE_P10; 11.
PROSITE; PS50208; CASPASE_P20; 1.
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InterPro; IPR002138; ICE_p10.
InterPro; IPR001309; ICE_p20.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    or send an email to license@isb-sib.ch).
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                                                                                            301
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SIMILARITY: BELONGS TO PEPTIDASE FAMILY C14.
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BY SIMILARITY.
CASPASE-7 SUBUNIT P11.
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EMBL; U67321; AAC53068.1; PEMBL; D86353; BAA19730.1; -EMBL; X13088; CAA73530.1; -EMBL; BC005428; AAH05428.1; HSSP; P42574; 1PAU.
                                                                                                                                                                                                                                                              use by non-profit institutions as long modified and this statement is not removed entitles requires a license agreement (See or send an email to license@isb-sib.ch).
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Juan T.S.-C., McNecce I.K., Argento J.M., Jenkins N.A., Gilbert D.J.
Copeland N.G., Fletcher F.A.;
Copeland I.G., Fletcher F.A.;
"Identification and mapping of Casp7, a cysteine protease resembling
CPP32 beta, interleukin-1 beta converting enzyme, and CED-3.";
Genomics 40:86-93(1997).
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Eukaryota; Metazoa; (
Mammalia; Eutheria; F
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van de Craen M., Vandenabeele P.,
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MEDLINE=97236307; PubMed=9125129;
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TISSUE=Skeletal muscle;
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CASP7 OR MCH3 OR LICE2.
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                                                nterPro;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     'Characterization of seven murine caspase family members.";
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 mitted (MAR-2001) to the EMBL/GenBank/DDBJ databases.
FUNCTION: INVOLVED IN THE ACTIVATION CASCADE OF CASPASES
RESPONSIBLE FOR APOPTOSIS EXECUTION: CLEAPES AND ACTIVATES STEROL
REGULATORY ELEMENT BINDING PROTEINS (SREBPS). OVEREXPRESSION
PROMOTES PROGRAMMED CELL DEATH (BY SIMILARITY).
SUBUNIT: HETERODIMER OF A 20 kDa (P20) AND A 11 kDa (P11) SUBUNIT.
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PTM: CLEAVAGES BY GRANZYME B OR CASPASE-10 GENERATE THE TWO ACTIVE SUBUNITS. PROPERTIDE DOMAINS CAN ALSO BE CLEAVED EFFICIENTLY BY
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SIMILARITY: BELONGS TO PEPTIDASE FAMILY C14.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      CPP32 PROTEASE. ACTIVE HETERODIMERS BETWEEN THE SMALL CASPASE-7 AND THE LARGE SUBUNIT OF CPP32 PROTEASE ALSO
                                         PS; C14.004; -. MGI:109383; Casp7 rpro; IPR002398; I
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IPR002138; ICE_p10.
IPR001309; ICE_p20.
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Rodentia;
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Sciurognathi; Muridae;
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P., van Criekinge
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Best Local
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WEDLINE-96183185; PubMed-8605870; Wang X., Zelenski N.G., Yang J., Sakai J., Brow Goldstein J.L.; "Cleavage of sterol regulatory element binding CPP32 during apoptosis.";
                                                                                                                      Cricetulus longicaudatus (Lon
Eukaryota; Metazoa; Chordata;
Mammalia; Eutheria; Rodentia;
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Q60431;
                                                                 TISSUE-Brain;
                                                                                                              Cricetulus
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01-NOV-1997 (Rel.
15-JUN-2002 (Rel.
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PROSITE; PS01121; CASPASE_HIS; 1.
PROSITE; PS50207; CASPASE_P10; 1.
PROSITE; PS50208; CASPASE_P20; 1.
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PROPEP
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Pfam; PF00656; ICE_p20; 1.
PRINTS; PR00376; IL1BCENZYME.
SMART; SM00115; CASC; 1.
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1 23 BY SIMILARITY.
24 198 CASPASE-7 SUBUNIT P20 (BY SIMILARITY).
199 206 BY SIMILARITY.
207 303 CASPASE-7 SUBUNIT P11 (BY SIMILARITY).
144 144 BY SIMILARITY.
186 186 BY SIMILARITY.
186 186 BY SIMILARITY.
190 11 EL -> DW (IN REF. 2).
45 45 A -> T (IN REF. 2).
46 49 VR -> RQ (IN REF. 2).
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35, Last sequence update)
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(EC 3.4.22.-) (Cysteine protease CPP32) (Yama (Caspase-3) (CASP-3) (SREBP Cleavage activity
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34060 MW;
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                                                                                                                      (Long-tailed hamster) (Chinese hamster).
data; Craniata; Vertebrata; Euteleostomi;
ntia; Sciurognathi; Muridae; Cricetinae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  27;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Score 1346; DB 1;
Pred. No. 4.4e-109;
7; Mismatches 29;
                                                                                                                                                                                                                                                       PRT;
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                                        Brown
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Best Local S
Matches 149
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Pfam; PF00656; ICE_p20; 1.

PRINTS; PR00376; IIIBCENZYME.

SMART; SM00115; CASC; 1.

PR0SITE; PS01122; CASPASE_CYS; 1

PR0SITE; PS01121; CASPASE_HIS; 1

PR0SITE; PS01207; CASPASE_P10; 1

PR0SITE; PS50208; CASPASE_P10; 1

PR0SITE; PS50208; CASPASE_P20; 1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   CHAIN
CHAIN
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            This SWISS-PROT entry is copyright. It is produced through between the Swiss Institute of Bioinformatics and the EN the European Bioinformatics Institute. There are no restruse by non-profit institutions as long as its content modified and this statement is not removed. Usage by an entitles requires a license agreement (See http://www.isb-s
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 <del>-</del> --
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 InterPro; IPR002398; ICE.
InterPro; IPR002138; ICE_p10.
InterPro; IPR001309; ICE_p20.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              MEROPS; C14.003;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         EMBL; U27463;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             or send an email to license@isb-sib.ch).
     230
                                                     256
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SUBCELLULAR LOCATION: Cytoplasmic.

PTM: CLEAVAGE BY GRANZYME B, CASPASE-6, -8 AND -10 GENERATES 7

TWO ACTIVE SUBUNITS. ADDITIONAL PROCESSING OF THE PROPERTIDES 1

LIKELY DUE TO THE AUTOCATALYTIC ACTIVITY OF THE ACTIVATED PROTEASE. ACTIVE HETERODIMERS BETWEEN THE SMALL SUBUNIT OF CASPASE-7 PROTEASE AND THE LARGE SUBUNIT OF CP932 ALSO OCCUR FULL VERSA (BY SIMILARITY).

SIMILARITY: BELONGS TO PEPTIDASE FAMILY C14.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          O J. 15:1012-1020(1996).

FUNCTION: INVOLVED IN THE ACTIVATION CASCADE OF CASPASES RESPONSIBLE FOR APOPTOSIS EXECUTION. AT THE ONSET OF APOPTOSIS IT PROTECLYTICALLY CLEAVES POLY(ADP-RIBOSE) POLYMERASE (PARP) AT A 216-ASP-|-GLY-217 BOND. CLEAVES AND ACTIVATES STEROL REGULATORY ELEMENT BINDING PROTEINS (SREBPS) BETWEEN THE BASIC HELIX-LOOPHELIX LEUCINE ZIPPER DOMAIN AND THE MEMBRANE ATTACHENT DOMAIN. CLEAVES AND ACTIVATES CASPASE-6, -7 AND -9 (BY SIMILARITY). SUBUNIT: HETERODIMER OF A 17 kDa (P17) AND A 12 kDa (P12) SUBUNIT.
                                                                                                                        LEFMHILTRVNRKVATEFESFSLDSTFHAKKQIPCIVSMLTKELYF
                                              LEIMQILTRVNDRVARHFESQSDDPHFHEKKQIPCVVSMLTKELYF
                                                                                              ETDSGTEDDMTCQ---KIPVEADFLYAYSTAPGYYSWRNPKDGSWFIQSLCSMLKLYAHK
                                                                                                                                                                                             CFACILLSHGEENVIYGKDGVTPIKDLTAHFRGDRCKTLLEKPKLFFIQACRGTELDDAI
                                                                                                                                                                                                                                                                                                                                                                                                                                              NEDSVDAKPDRSSFVPSLFSKKK--KNVTMRSIKTTRDRVPTYQYNMNFEKLGKCIIINN
                                                                                                                                                                                                                                                                                               KNFHKSTGMTPRSGTDVDAAKLRETFMALKYEVRNKNDLTREEIVELMKNASKEDHSKRS
                                                                                                                                                                                                                                                                                                                      KNFDKVTGMGVRNGTDKDAEALFKCFRSLGFDVIVYNDCSCAKMQDLLKKASEEDHTNAA
                                                                                                                                                                                                                                                                                                                                                                                                NETSVDSKSIKNFEVKTIHGSKSMDSGIYLDS---
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149; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           163
277
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28
175
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9 BY SIMILARITY.
28 BY SIMILARITY.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           46.1%;
52.1%;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       APOPAIN P17 SUBUNIT.
APOPAIN P12 SUBUNIT.
BY SIMILARITY.
BY SIMILARITY.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Score 744; DB 1;
Pred. No. 4.1e-57;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                OBF3A4590A2828A3 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Mismatches
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Lee D., Long S.A., Adams J.L., Chan G., Vaidya K.S., Francis T.A., Kikly K., Winkler J.D., Sung C.-M., Debouck C., Richardson S., Levy M.A., DeWolf W.E. Jr., Keller P.M., Tomaszek T., Head M.S., Ryan M.D., Haltiwanger R.C., Liang P.-H., Janson C.A., McDevitt P. Johanson K., Concha N.O., Chan W., Abdel Meguid S.S., Badger A.M., Johanson K., Nadeau D.P., Suva L.J., Gowen M., Nuttall M.E., "Potent and selective nonpeptide inhibitors of caspases 3 and 7 inhibit apoptosis and maintain cell functionality.";
                                                                                                                                                                                                                X-RAY CRYSTALLOGRAPHY (2.8 ANGSTROMS). MEDLINE=20283632; PubMed=10821855;
                                                                                                                                                                                                                                                                                       Mittl P.R., di Marco S., Krebs J.F., Bai X., Kare Priestle J.P., Tomaselli K.J., Grutter M.G., "Structure of recombinant human CPP32 in complex tetrapeptide acetyl-Asp-Val-Ala-Asp fluoromethyl J. Biol. Chem. 272:6539-6547(1997).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Nicholson D.W., Ali A., Thornberry N.A., Vaillancon Gallant M., Gareau Y., Griffin P.R., Labelle M., Lamunday N.A., Raju S.M., Smulson M.E., Yamin T.-T.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        MEDLINE-95292347; PubMed-7774019;
Tewari M., Quan L.T., O'Rourke K., Desnoyers S., Zeng Z.,
Beidler D.R., Poirier G.G., Salvesen G.S., Dixit V.M.;
"Yama/CPP32 beta, a mammalian homolog of CED-3, is a CrmA-inhibitable
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Thornberry N.A., Becker J.W.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    MEDLINE-95319529;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 SEQUENCE
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"CPP32, a novel human apoptotic protein with
Caenorhabditis elegans cell death protein Cec
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  01-NOV-1995 (Rel.
01-NOV-1995 (Rel.
15-JUN-2002 (Rel.
                                                                                                                                                                                                                                           X-RAY CRYSTALLOGRAPHY (2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       MEDLINE=96266352; PubMed=8673606
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Miller D.K.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              protease that cleaves the death
                                                                                                                                                                                                                                                                                                                                                                                                                           MEDLINE-97197830;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Eukaryota; Metazoa;
Mammalia; Eutheria;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Apopain precursor protein) (CPP-32)
                                                                                                                                                                                                                                                                                                                                                                                                                                                 (-RAY CRYSTALLOGRAPHY (2.3 ANGSTROMS)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Labelle M.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 (-RAY CRYSTALLOGRAPHY (2.5
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Identification and inhibition of the
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         interleukin-1 beta-converting enzyme.
J. Biol. Chem. 269:30761-30764(1994).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        MEDLINE=95074098; PubMed=7983002;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            NCBI_TaxID=9606;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      mammalian apoptosis.";
ure 376:37-43(1995).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                three-dimensional structure of apopain/CPP32, a key mediator of
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Struct.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           81:801-809(1995).
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Metazoa; Chordata; C
Metazoa; Primates; (
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Nicholson D.W., Fazil K.M., Peterson E.P., Rasper D.M.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            29-46 AND 175-193,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Biol.
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                                                                                                                                                                                                                                                                                                                                                                                                                           PubMed=9045680;
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41, Last annotation update)
(EC 3.4.22.-) (Cysteine pro
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                (EC 3.4.22.-) (Cysteine protease CPP32) (Yama (Caspase-3) (CASP-3) (SREBP cleavage activity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     3:619-625(1996)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          (ALPHA AND
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Catarrhini;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ICE/CED-3 protease necessary
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Gallant M., Ruel R., Va
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Vertebrata; Euteleostomi;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Vaillancourt J.P., Din
elle M., Lazebnik Y.A.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                   35-173 AND
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poly(ADP-ribose)
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                                                                                                                                                                                                                                                                                                                                                                                            Karanewsky D.
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                                                                                                                                                                                                                                                                                                                    ketone.";
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Hydrolase; Th 3D-structure.

Thiol protease;

Zymogen;

Apoptosis; Polymorphism,

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PRINTS; PRO0376; ILLBCENZYME.
SMART; SM00115; CASC; 1.
PROSITE; PS01122; CASPASE_CYS; 1
PROSITE; PS01121; CASPASE_HIS; 1
PROSITE; PS50207; CASPASE_P10; 1
PROSITE; PS50208; CASPASE_P20; 1
                                                                                                                                                                                                                                                              EMBL;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Pfam; PF00655; ICE_p10; 1. Pfam; PF00656; ICE_p20; 1.
                                                                                                                                                                                                                                     PDB;
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                                                                                                                                                                            MIM;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  "In vitro activation of CPP32 and Mch3 by Mch4, a novapoptotic cysteine protease containing two FADD-like Proc. Natl. Acad. Sci. U.S.A. 93:7464-7469(1996).
                                                                                                                                      InterPro;
                                                                                                                                                  InterPro;
                                                                                                                                                               [nterPro;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                 ENZYME REGULATION: INHIBITED BY ISATIN SULFONAMIDES.
SUBUNIT: HETERODIMER OF A 17 kDa (P17) AND A 12 kDa (P12) SUB
SUBCELLULAR LOCATION: Cytoplasmic.
TISSUE SPECIFICITY: HIGHLY EXPRESSED IN LUNG, SPLEEN, HEART,
AND KIDNEY. MODERATE LEVELS IN BRAIN AND SKELETAL MUSCLE, AND
IN TESTIS. ALSO FOUND IN MANY CELL LINES, HIGHEST EXPRESSION
CELLS OF THE IMMUNE SYSTEM.
PYM: CLEAVAGE BY GRANZYME B, APAF-1, CASPASE-6, -8 AND -10
GENERATES THE TWO ACTIVE SUBUNITS. ADDITIONAL PROCESSING OF THE PROPERTIDES IS LIKELY DUE TO THE AUTOCATALYDE CACTIVITY OF THE
PROPERTIDES IS LIKELY DUE TO THE AUTOCATALYDE CHEMICAND.
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                                                                                                                                                                                                                                                                                                                                                     European Bioinformatics Institute.
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1CP3; 24-DEC-97.
1GFW; 23-JUN-00.
                                                                                                                                                                        600636;
                                                                                                                                                                                                                                                                                                                                                                                                        SIMILARITY:
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                                                                                                                                                                                                                                                                                                                                                                                                                   AND
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    CLEAVAGE OF HUNTINGTIN
                                                                                                                                                                                                                                                                                                                                                                                                                                             ACTIVATED PROTEASE. ACTIVE HETERODIMERS BETWEEN THE SMALL SUBUNIT
                                                                                                                                                                                                                                                                                                                                                                SWISS-PROT entry is copyright. It is produced through sen the Swiss Institute of Bioinformatics and the EN
                                                                                                                                                                                                                                                U13737; AAA65015.1;
U13738; AAB60355.1;
U26943; AAA74929.1;
                                                                                                                                                                                     HGNC: 1504;
                                                                                                                                                                                                                                                                                                                                                                                                                   CASPASE-7 PROTEASE AND THE LARGE SUBUNIT OF CPP32 ALSO OCCURD VICE VERSA.
                                                                                                                                                                                                                                                                                                                                         non-profit
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Bullrich F.,
                                                                                                                                   IPR002138;
IPR001309;
                                                                                                                                                            IPR002398;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    275:16007-16014(2000).
                                                                                                                                                                                                                                                                                                                                                                                                        BELONGS TO PEPTIDASE FAMILY C14.
                                                                                                                                                                                      CASP3
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   PubMed=8755496;
T., Armstrong R.
F., Fritz L.C.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  PubMed=8696339;
cholson D.W., Rasper
                                                                                                                                                                                                                                                                                                                                       institutions as long as its content
                                                                                                                                   ICE_p20
                                                                                                                                                 ICE_p10
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Trapani J.A.,
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Tomaselli K.J.,
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MBL outstation -
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Best Local
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                                 Flaws J.A., Kugu K., Trbovich A.M., Desanti A., Tilly K.I., Hirshfield A.N., Tilly J.L.;

"Interleukin-1 beta-converting enzyme-related proteases (IRPs) and mammalian cell death: dissociation of IRP-induced oligonucleosomal endonuclease activity from morphological apoptosis in granulosa cell of the ovarian follicle.";

Endocrinology 136:5042-5053(1995).
TISSUE-Brain;
MEDLINE-97184204; PubMed-9030616;
                                                                                                                                       and
                                                                                                                                                                                                                                             15-JUN-2002 (Rel. 35, Last sequence update)
15-JUN-2002 (Rel. 41, Last annotation update)
Apopain precursor (EC 3.4.22.-) (Cysteine protease CPP32) (Yama protein) (CPP-32) (Caspase-3) (CASP-3) (SREBP cleavage activity (SCA-1) (LICE) (IRP).
                                                                                                                        Oncogene [2]
                                                                                                                                             a cysteine protease
                                                                                                                                                                      Juan T
                                                                                                                                                                                                               Rattus norvegicus (Rat).
Eukaryota; Metazoa; Chordata;
Mammalia; Eutheria; Rodentia;
                                                                                                                                                                                                                                                                      P55213; P70543; Q62993;
01-OCT-1996 (Rel. 34, C)
01-NOV-1997 (Rel. 35, Ld
15-JUN-2002 (Rel. 41, Ld
                    SEQUENCE FROM N.A
                                                                                            MEDLINE=96042508; PubMed=7588240;
                                                                                                       TISSUE-Ovary;
                                                                                                                                                                Fletcher F.A.;
                                                                                                                                                                               MEDLINE=96358624;
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                                                                                                                                                      Molecular characterization
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         143;
                                                                                                                                                                       .S.-C., McNiece
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Similarity
                                                                                                                             13:749-755(1996)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         277
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29
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121
163
190
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                                                                                                                                                                                                                                                                                                          STANDARD;
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175
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APOPAIN P12 SUBUNIT.
BY SIMILARITY.
BY SIMILARITY.
D -> E (IN ISOPORM BETA).
                                                                                                                                                                     Jenkins N.A.,
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                                                                                                                                                                                                             Craniata; Vertebrata; Euteleostomi; Sciurognathi; Muridae; Murinae; Rat
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                /FTId=VAR_001401
                                                                                                                                                                                                                                                                                                          PRT;
                                                                                                                                             mouse and rat interleukin-1
                                                                                                                                                      mouse
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                                                                                                                                                                    Gilbert D.J.,
                                                                                                                                             CPP32 beta gene beta converting
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or send an email to license@isb-sib.ch).
                                                                                                                                                     the European Bioinformatics Institute.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Submitted (JUN-1996)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            SEQUENCE OF 1-264 FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            apoptosis
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                                                                                                                                                                                                                                                                                                                  PTM: CLEAVAGE BY GRANZYME B, CASPASE-6, -8 AND -10 GENERATES 1 TWO ACTIVE SUBUNITS. ADDITIONAL PROCESSING OF THE PROPERTIDES LIKELY DUE TO THE AUTOCATALYTIC ACTIVITY OF THE ACTIVATED PROTEASE. ACTIVE HETERODIMERS BETWEEN THE SMALL SUBUNIT OF CASPASE-7 PROTEASE AND THE LARGE SUBUNIT OF CPP32 ALSO OCCUR & VICE VERSA (BY SIMILARITY).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 mitted (JUN-1996) to the EMBL/GenBank/DDBJ databases.
FUNCTION: INVOLVED IN THE ACTIVATION CASCADE OF CASPASES
RESPONSIBLE FOR APOPTOSIS EXECUTION. AT THE ONSET OF APOPTOSIS IT
PROTECLYTICALLY CLEAVES POLY(ADP-RIBOSE) POLYMERASE (PARP) AT A
216-ASP-1-GLY-217 BOND. CLEAVES AND ACTIVATES STEROL REGULATORY
ELEMENT BINDIAG PROTEINS (SREBPS) BETWEEN THE BASIC HELLY-LOOP-
HELLX LEUCINE ZIPPER DOMAIN AND THE MEMBRANE ATTACHMENT DOMAIN.
CLEAVES AND ACTIVATES CASPASE-6, -7 AND -9 (BY SIMILARITY).
SUBUNIT: HETERODIMER OF A 17 kDa (P17) AND A 12 kDa (P12) SUBUNIT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 (BY SIMILARITY).
SUBCELLULAR LOCATION: Cytoplasmic.
TISSUE SPECIFICITY: EXPRESSED IN HEART,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ADULT BRAIN.
PTM: CLEAVAGE BY GRANZYME
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         BUT NOT IN KIDNEY OR TESTIS.

DEVELOPMENTAL STAGE: HIGHLY EXPRESSED IN NEURON-ENRICHED OF THE DEVELOPING BRAIN, BUT DOWN-REGULATED TO LOW LEVELS
                                                                                                                                             SWISS-PROT entry is copyright. It is produced through a collaboration een the Swiss Institute of Bioinformatics and the EMBL outstation - Buropean Bioinformatics Institute. There are no restrictions on its
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      cultured cerebellar granule neurons."; 17:1561-1569(1997).
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Pfam; PF00655; ICE_D10; 1.
Pfam; PF00655; ICE_D20; 1.
Pfam; PF00656; ICE_D20; 1.
PRINTS; PR00376; ILIBCENZYME.
SMART; SM00115; CASC; 1.
SMO0115; PS01122; CASPASE_CYS; 1
PROSITE; PS01121; CASPASE_HIS; 1
PROSITE; PS050207; CASPASE_P10; 1
PROSITE; PS50207; CASPASE_P00; 1
PROSITE; PS50208; CASPASE_P00; 1 CHAIN
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CONFLICT
CONFLICT EMBL; U49930; EMBL; U34685; EMBL; U84410; EMBL; U58656; EMBL; U58656; PROPEP PROPEP Hydrolase; InterPro; IPR002398; ICE. InterPro; IPR002138; ICE_p10 InterPro; IPR001309; ICE_p20 MEROPS; C14. 10 29 176 121 163 25 170 178 187 187 199 .003; AAC52261.1; AAB41792.1; AAB02722.1; 1PAU AAC52765.1; protease; 28 175 277 121 163 29 170 178 182 182 187 199 Zymogen; Zymogen; Apoptosis.
BY SIMILARITY.
BY SIMILARITY.
BY SIMILARITY.
APOPAIN P17 SUBUNIT.
APOPAIN P12 SUBUNIT.
BY SIMILARITY.
BY SIMILARITY. KSMDS

T -> F

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T -> F

T -> F -> QVD S (IN RE A (IN RI V (IN R K (IN F G (IN I S (IN REF. REF. REF. REF. REF. (IN REF. ٥.

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Best Local
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01-NOV-1997
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CONFLICT
SEQUENCE
                                                              STRAIN=Con,....
MEDLINE=97190206; PubMeu-----
van de Craen M., Vandenabeele
van de Craen M., Schot
                                                                                                                                                                                                                                                                                                                                                                                                                                                               vi-NOV-1997 (Rel. 35, Created)
01-NOV-1997 (Rel. 35, Last seq
15-JUN-2002 (Rel. 41, Last ann
Anomain recommendations)
                                                                                                                                                             activation
NGF.";
                                                                                                                                                                       Mukasa T., Urase K., Momoi M.Y., Kimura I., Momoi T.; "Specific expression of CPP32 in sensory neurons of mouse embryos and activation of CPP32 in the apoptosis induced by a withdrawal of
                                                                                                                                                                                                                                                                  and
                                                                                                                                                                                                                                                                                                                Juan T.S.-C., McNiece
                                                                                                                                                                                                                                                                                                                                                                           Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus
                                                                                                                                                                                                                                                                                                                                                                                                     Mus musculus (Mouse)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   MOUSE
         SEQUENCE FROM N.A
                                  FEBS Lett.
                                                                                                                       SEQUENCE FROM N.A.
                                                                                                                                                Biochem. Biophys.
                                                                                                                                                                                                                          SEQUENCE FROM
                                                                                                                                                                                                                                                   Oncogene 13:749-755(1996).
                                                                                                                                                                                                                                                                                                     Fletcher F.A.;
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                                                                                                                                                                                                                                                                                                                                                                                                                       CASP3 OR CPP32
                                                            Fiers W.;
                                                                                                                                                                                                            MEDLINE=97224429; PubMed=9070890;
                                                                                                                                                                                                                                                                                                                                                                   NCBI_TaxID=10090;
                                                                                                                                                                                                                                                                                       Molecular characterization of
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      SFVCVILSHGDEGVIFGTNGPVDLKKLTSFFRGDYCRSLTGKPKLFIIQACRGTELDCGI 172
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           008668;
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245
277
                                  ization of seven murine 403:61-69(1997).
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                                                                                                                                                                                                                                                                                                                                                                                                                                        41, Last annotation update)
(EC 3.4.22.-) (Cysteine protease CPP32) (Yama (Caspase-3) (CASP-3) (SREBP cleavage activity
                                                                                             PubMed=9038361;
                                                                                                                                                 Res.
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245
31491 MW;
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                                                                                                                                                Commun.
                                                                     Schotte P.,
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                                                                                                                                                                                                                                                                                                                Jenkins N.A.,
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                                                                                                                                                                                                                                                                                      mouse and rat CPP32 beta gene
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-> M (IN REF. 3).
ADABF418E2507402 CRC64;
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                                                                    Declercq W., van
P., van Criekinge
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                                            caspase family members.";
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No. 1.1e-54;
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                                                                     Brande I.,
Beyaert R.,
                                                                                                                                                                                                                                                                                                                Copeland N.G.
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EMBL;
HSSP; P42574;
MEROPS; C14.003;
MGROPS; C14.003;
MGD; MGI:107739; Casp3.
InterPro; IPR002398; ICE_P10.
InterPro; IPR002138; ICE_p10.
'Pro; IPR001309; ICE_p20.
'Pro; ICE_P10; 1.
'Pro; ICE_P10; 1.
'Pro; ICE_P10; 1.
            CHAIN
ACT_SITE
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PROSITE; PS01121; CASPASE_HIS;
PROSITE; PS50207; CASPASE_P10;
PROSITE; PS50208; CASPASE_P20;
                                                                                                                                                                                                                                                                                                                                                                                                                                                           EMBL; U54802; AACS2768.1; JOINED.
EMBL; U49929; AACS2764.1; -.
EMBL; D86352; BAA21727.1; -.
EMBL; X13086; CAA73528.1; -.
                                                                                                                                                                   CHAIN
                                                                                                                                                                                                                                                                                          PRINTS; PR00376; IL1BCENZYME SMART; SM00115; CASC; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     use
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  the European Bioinformatics Institute.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Fernandes-Alnemri T., Litwack G., Alnemri E.S.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           mitted (MAY-1997) to the EMBL/GenBank/DDBJ databases.
FUNCTION: INVOLVED IN THE ACTIVATION CASCABOR
FUNCTION: INVOLVED IN THE ACTIVATION CASCABOR
RESPONSIBLE FOR APOPTOSIS EXECUTION. AT THE ONSET OF APOPTOSIS IT
PROTEOLYTICALLY CLEAVES POLY(ADP-RIBOSE) POLYMERASE (PARP) AT A
216-ASP-1-GLY-217 BOND. CLEAVES AND ACTIVATES STEROL REGULATORY
ELEMENT BINDING PROTEINS (SREBPS) BETWEEN THE BASIC HELIX-LOOP-
HELIX LEUCINE ZIPPER DOMAIN AND THE MEMBRANE ATTACHMENT DOMAIN.
CLEAVES IL-1 BETA BETWEEN AN ASP AND AN ALA, RELEASING THE MATURE
CYTOKINE WHICH IS INVOLVED IN A VARIETY OF INFLAMMATORY PROCESSES.
SUBGUST: HETERODIMER OF A 17 kDa (P17) AND A 12 kDa (P12) SUBGUST
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             PTM: CLEAVAGE BY GRANZYME B, CASPASE-5, -8 AND -10 GENERATH TWO ACTIVE SUBUNITS. ADDITIONAL PROCESSING OF THE PROPEPTIL LIKELY DUE TO THE AUTOCATALYTIC ACTIVITY OF THE ACTIVATED PROTEASE. ACTIVE HETERODIMERS BETWEEN THE SMALL SUBUNIT OF CASPASE-7 PROTEASE AND THE LARGE SUBUNIT OF CPP32 ALSO OCCUSANDED VICE VERSA (BY SIMILARITY).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               (BI SIMALIFANTAN),
SUBCELLULAR LOCATION: CYCOplasmic.
TISSUE SPECIFICITY: HIGHEST EXPRESSION IN SPLEEN, LUNG, LIVER,
TISSUE SPECIFICITY: HIGHEST EXPRESSION IN BRAIN, SKELETAL MUSCLE AND
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               SWISS-PROT entry is copyright. It is producen the Swiss Institute of Bioinformatics
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31474 MW;
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APOPAIN P17 SUBUNIT
APOPAIN P12 SUBUNIT
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N -> T (IN REF: 2).
Q -> E (IN REF: 2).
L -> M (IN REF: 2).
L -> M (IN REF: 2).
Y -> F (IN REF: 2).
Y -> F (IN REF: 2).
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CRC64;
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Matches 146;

Query Match Best Local

Similarity

43.6%;

Score Pred.

Conservative

40;

ore 703; Ded. No. 1.4 Mismatches

Indels

18;

Gaps

DB 1; 4e-53;

Length 277;

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RESULT
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PRINTS; PROUL
SMART; SMOOLLS; CAS
                                                                                                                                                                                                                                                                                                                                                            Yaoita Y., Nakajima K.;

"Induction of apoptosis and CPP32 expression by thyroid hormone in a myoblastic cell line derived from tadpole tail.";

J. Biol. Chem. 272:5122-5127(1997).

-i- FUNCTION: IMPORTANT MEDIATOR OF APOPTOSIS. AT THE ONSET OF APOPTOSIS IT PROTEOLYTICALLY CLEAVES POLY(ADP-RIBOSE) POLYMERASE (PARP) AT A 216-ASP-|-GLY-217 BOND (BY SIMILARITY).

-i- SUBUNIT: HETERODIMER OF A 17 kDa (P17) AND A 12 kDa (P12)
                                 Pfam; PF00655; ICE_P10; 1.
Pfam; PF00656; ICE_P20; 1.
PRINTS; PR00376; ILIBCENZYME
                                                                                                                                                 EMBL;
                                                                                                                                                                        use by non-profit institutions as long modified and this statement is not removed. entities requires a license agreement (See or send an email to license@isb-sib.ch).
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01-NOV-1997 (Rel. 35,
15-JUN-2002 (Rel. 41,
Apopain precursor (EC
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                                                                                                                        MEROPS; C14.003;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Eukaryota;
                                                                                InterPro;
                                                                                            InterPro;
                                                                                                          InterPro;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   MEDLINE=97184166;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          NCBI_TaxID=8355;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Xenopodinae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Xenopus laevis (African clawed frog).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Amphibia; Batrachia;
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                                                                                                                                                                                                             S SWISS-PROT entry is copyright. It is produced through a collabween the Swiss Institute of Bioinformatics and the EMBL outst European Bioinformatics Institute. There are no restrictions by non-profit institutions as long as its content is in
                                                                                                                                                                                                                                                                                    OTHER CASPASES (BY SIMILARITY). SIMILARITY: BELONGS TO PEPTIDASE FAMILY C14.
                                                                                                                                                                                                                                                                                             SUBCELLULAR LOCATION: Cytoplasmic (By similarity).
MISCELLANEOUS: THE SUBUNITS ARE DERIVED FROM THE PRECURSOR SEQUENCE BY A PROBABLE AUTOCATALYTIC MECHANISM AND PROBABL OTHER CASPASES (BY SIMILARITY).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            CFACILLSHGEENVIYGKDGVTPIKDLTAHFRGDRCKTLLEKPKLFFIQACRGTELDDAI 195
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        KLEFMHILTRVNRKVATEFESFSLDSTFHAKKQIPCIVSMLTKELYF
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                                                                                                                                      P42574;
                                                                                                                                                D89784; BAA14018.1;
                                                                             IPR002138; ICE_p10
IPR001309; ICE_p20
                                                                                                        IPR002398; ICE.
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                            CASc;
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            CASPASE_CYS;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 PubMed=9030578;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Anura; Mesobatrachia;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Created)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              update;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       282
                                                                                                                                                                                   (See http://www.isb-sib.ch/announce/
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  update)
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ICE1_SPOFR
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                        use by modified
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                                                             This SWISS-PROT entry is copyright. It is produced through between the Swiss Institute of Bioinformatics and the Enthe European Bioinformatics Institute. There are no restricted the succession of the succession
                                                                                                                                                                                                                                         "Spodoptera frugiperda caspase-1, a novel insect death protect cleaves the nuclear immunophilin FKBP46, is the target of the baculovirus antiapoptotic protein p35.";
J. Biol. Chem. 272:1421-1424(1997).
-i- FUNCTION: INVOLVED IN THE ACTIVATION CASCADE OF CASPASES
-i- FUNCTION: INVOLVED IN THE ACTIVATION (BY SIMILARITY). INHITHE BACULOVIRUS ANTI-APOPTOTIC PROTEIN P35. CLEAVES P35. NUCLEAR IMMUNOPHILIN FKBP46.
                                                                                                                                                                                                                                                                                                                                                                                                                                     SEQUENCE FROM N.A., AND PARTIAL SEQUENCE.
MEDLINE=97153084; PubMed=8999805;
Ahmad M., Srinivasula S.M., Wang L., Litwack G.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ACT_SITE
ACT_SITE
SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Eukaryota; Metazoa; Arthropoda; Mandibulata; Pancrustacea; Insecta; Pterygota; Neoptera; Endopterygota; Lepidoptera; Olitrysia; Noctuoidea; Noctuoidea; Amphipyrinae; Spodoptera.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          01-NOV-1997 (Rel. 35, Created)
01-NOV-1997 (Rel. 35, Last Sequence update)
15-JUN-2002 (Rel. 41, Last annotation update)
Caspase-1 precursor (EC 3.4.22.-).
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01-NOV-1997 (Rel.
15-JUN-2002 (Rel.
                                                                                                                                                                                                                                                                                                                                                                                                                         Alnemri E.S.
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                                                                                                                                                   PTM: AN AUTOCATALYTIC MECHANISM GENERATES THE TWO SIMILARITY: BELONGS TO PEPTIDASE FAMILY C14.
                                                                                                                                                                                                  SUBUNIT.
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non-profit institu
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requires a license
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CASPASE_P20;
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282 A
131 B
174 B
32124 MW;
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APOPAIN P12 SUBUNIT.
BY SIMILARITY.
BY SIMILARITY.
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No. 4.7e-50;
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Best Local Similarity
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                                                                                                                              Oli382; GyVAHI;
Oli382; GyVAHI;
11-NOV-1997 (Rel. 35, Created)
116-OCT-2001 (Rel. 40, Last sequence update)
15-JUN-2002 (Rel. 41, Last annotation updat)
15-JUN-2002 (Rel. 41, Last annotation updat)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ACT_SITE
ACT_SITE
SEQUENCE
  "Identification
                                                                     Drosophila melanogaster (Fruit fly).

Eukaryota; Metazoa; Arthropoda; Mandibulata; Pancrustacea; Hexapoda; Insecta; Pterygota; Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha; Ephydroidea; Drosophilidae; Drosophila.

NCBI_TaxID=7227;
               TISSUE-Embryo;
MEDLINE-97327558; PubMed-9184225;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    CHAIN
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InterPro;
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                                               SEQUENCE FROM N.A.
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                                                                                                                                                                                                                                                                                                                                                                                                                                      ASEEDHTNAACFACILLSHGEENVIYGKDGVTPIKDLTAHFRGDRCKTLLEKPKLFFIQA 185
                                                                                                                                                                                                                                                                                                                                                                                                                                                              HRGMAIIFNHEHFD-IHSLKSRTGTNVDSDNLSKVLKTLGFKVTVFPNLKSEEINKFIQQ
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      KLGKCIIINNKNFDKVTGMGVRNGTDKDAEALFKCFRSLGFDVIVYNDCSCAKMQDLLKK 125
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             Evan G.I.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Conservative
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                                                                                                                                                                                                         STANDARD;
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184
195
299
136
178
33527
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Drosophila melanogaster ICE/CED-3-related
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               52;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Score 552; DB
Pred. No. 1.8e
52; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       CASPASE-1 SUBUNIT
BY SIMILARITY.
BY SIMILARITY.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             CASPASE-1 SUBUNIT P19/18. POTENTIAL.
                                                                                                                                                                                                         PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             99F4FED09B04EEDE CRC64
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                                                                                                                                                                                                         339
                                                                                                                                                         update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         DB 1;
.8e-40;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  P12
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Length 299
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RA HOSTID D. HOUSTON K.A. HOWLAND J.W. M. M. H. TIDEGWAMD C. A. HOSTID D. HOUSTON K.A. HOWLAND J. W. M. H. TIDEGWAMD C. A. RA HOSTID D. HOUSTON K.A. HOWLAND J.A. KETCHUM K.A. RA KIMMEL B.E. KOGLICA C.D. KRAFT C., KRAVITZ S., KULP D., LAI 2. RA KIMMEL B.E. KOGLICA C.D., KRAFT C., KRAVITZ S., KULP D., LAI 2. RA LISKO P., LEI Y., LEVILSKY A.A., LI J. LI Z., LIANG Y. LIAN X. RA LIN X., MATTEN B., MCINTOSH T.C., MCLEOOM M.P., MCPHERSON D.L., RA MCHINT S.M., MOY M., MUTPHY B., MUTPHY L., MUZHY D.M., NOLSON D.L., RA NELSON D.R., NELSON K.A., NIXON K., NUSSKERN D.R., PACLED J.M., NALSON D.L., RA PALAZZOLO M., PIKTMAN G.S., PAN S., POLLARD J., PUTI V., REESE M.G., RA PALAZZOLO M., PIKTMAN G.S., PAN S., POLLARD J., PUTI V., REESE M.G., RA PALEZZOLO M., PIKTMAN G.S., PAN S., VENDLARD J., PUTI V., REESE M.G., RA SPIER E., SPRAGLING A.C., STAPLETON M., SKUPSKI M.P., SMITH T., RANG Y., WASSATMAN D.A., WeINSTOCK G.M., WELSSENDACH J., RA WANG Z.-Y. WASSATMAN D.A., WEINSTOCK G.M., WELSSENDACH J., RA YE J., YEH R.-F., Zaveri J.S., Zhan M., Zhang G., Zhao Q., Zheng X.H., Kang S.H., Wang S.H., Wang S.H., Wang S.H., Wang Y.H., Zhong F.N., Zhong W., Zhou X., Zhu S., Zhu X., SMITH H.O., RA YE J., YEH R.-F., Zhveri J.S., Zhu X., Zhu S., Zhu X., SMITH H.O., RA YE J., YE PALEZZOLO J. NOTON J. ZHU X., SMITH H.O., RA YE J., YE PALEZZOLO J. THE ACTIVATION CASCADE OF CASPASES C. C. CLEAVES BACCULOURING P.S. AND LAMIN DMO IN VITRO.

CC. CLEAVES BACCULOURING P.S. AND LAMIN DMO IN VITRO.

CC. CLEAVES BACCULOURING P.S. AND LAMIN DMO IN VITRO.

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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Fosler C., Gabrielian A.E., Garg N.S., Gelbart W.M., Glasser K., Glodek A., Gong F., Gorrell J.H., Gu Z., Guan P., Harris M., Glodek A., Harvey D., Heiman T.J., Hernandez J.R., Houck J.,
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Fosler
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Sutton G.G., Wortman J.R., Yandell M.D., Zhang Q., Chen Brandon R.C., Rogers Y.-H.C., Blazej R.G., Chambe M. D. Wan K.H., Dovie C.
                     PRINTS; PR00376
SMART; SM00115;
                                                                  Pfam; PF00655; Pfam; PF00656;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Cherry J.M., Cawley S., Dahlke C., Davenport L.B., Davies P., de Pablos B., Delcher A., Deng Z., Mays A.D., Dew I., Dietz S. Dodoson K., Doup L.E., Downes M., Dugan-Rocha S., Dunkov B.C., Durbin K.J., Evangelista C.C., Ferraz C., Ferriera S., Fleisci
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Beeson K.Y., Benos P.V., Berman B.P., Bhandari D., Bolshako
Borkova D., Botchan M.R., Bouck J., Brokstein P., Brottier
Burtis K.C., Busam D.A., Butler H., Cadieu E., Center A., (
                                                                                                                                                                                                                                                EMBL; X12261; CAA72937.1; ... EMBL; AE003771; AAF56939.1;
                                                                                                                                                                                                                                                                                                                     entities requires a license agreement (S or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                               use by non-profit institutions as long modified and this statement is not removed
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Brandon R.C., Rogers Y.-H.C., Blazej R.G., Champe M., Pfeiffen Wan K.H., Doyle C., Baxter E.G., Helt G., Nelson C.R., Miklos Abril J.F., Agbayani A., An H.-J., Andrews-Pfannkoch C., Baldw
PROSITE; PS01122;
                                                                                                                                                                                  FlyBase; FBgn0019972;
                                                                                                                                                                                                     MEROPS; C14.015;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Beeson K.Y.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Adams M.D., Celn
Amanatides P.G.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     MEDLINE=20196006;
                                                                                                                                                          InterPro;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    EMBO
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       SIMILARITY: BELONGS TO PEPTIDASE FAMILY C14.
                                                                                                                                                                                                                               P42574;
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                                                                                                          : IPR002398;
: IPR002138;
: IPR001309;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        .M., Basu A., Baxendale J., Bayraktaroglu L., Beasley E.M., Y., Benos P.V., Berman B.P., Bhandari D., Bolshakov S.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Celniker S.E., Holt R.A., Ev
P.G., Scherer S.E., Li P.W.,
Lewis S.E., Richards S., As
                                        ; ICE_p10; 1.
; ICE_p20; 1.
76; IL1BCENZYME.
                                                                                                                                                                                                                               1PAU.
                       CASc;
CASPASE_CYS;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     PubMed=10731132;
                                                                                                          ICE_p10.
ICE_p20.
                                                                                                                                                                                                                                                                                                                                                                                  rmatics Institute. There are no rest
institutions as long as its content
                                                                                                                                                                                                                                                                                                                                        (See http://www.isb-sib.ch/announce/
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Evans C.A.,
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                                                                                                                                                                                                                                                                                                                                                               Usage
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., Galle R.F.,
Henderson S.N.,
                                                                                                                                                                                                                                                                                                                                                                                                          restrictions
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                                                                                                                                                                                                                                                                                                                                                                                                                                       a collaboration
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Dunn
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Best Loc
Matches
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[2]
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ACT_SITE
CONFLICT
CONFLICT
Adams M.D., Celniker S.E., Holt R.A., Evans C.A., Gocayne J.D. Amanatides P.G., Scherer S.E., Li P.W., Hoskins R.A., Galle R. George R.A., Lewis S.E., Richards S., Asburner M., Henderson Sutton G.G., Wortman J.R., Yandell M.D., Zhang Q., Chen L.X., Brandon R.C., Rogers Y.-H.C., Blazej R.G., Champe M., Pfeiffer
                                                                                                                                                                                    Song
                                                                                                                                                                                                                                                                                                                                                                                                DROME
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       PROPEP
                                                   STRAIN=Berkeley;
MEDLINE=20196006; PubMed=10731132;
                                                                                                                                                                                              TISSUE=Embryo;
MEDLINE=97153052;
                                                                                                                                                                                                                                                                                Drosophila melanogaster (Fruit fly).
Eukaryota; Metazoa; Arthropoda; Mandibulata; Pancrustacea; Hexapoda;
                                                                                                                                                                                                                                                                                                         Caspase-1 precursor (EC DCP-1 OR CG5370.
                                                                                                                                                                                                                                                                                                           )02002; (yww.n.,
15-JUL-1998 (Rel. 36, Last sequence update)
15-JUN-2002 (Rel. 41, Last annotation updat
15-JUN-2002 (Rel. 41, Cast annotation updat)
                                                                                                                                                                                                                                                                                                                                                        002002; Q9W1NO;
15-JUL-1998 (Rel.
                                                                                                                                                                                                                                              Muscomorpha; Ephydroidea;
NCBI_TaxID=7227;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  CHAIN
                                                                                   SEQUENCE FROM N.A.
                                                                                                             Science
                                                                                                                         Song
                                                                                                                                     ERRATUM.
                                                                                                                                                                                                                      SEQUENCE FROM N.A.,
                                                                                                                                                                                                                                                         Insecta; Pterygota; Neoptera; Endopterygota; Diptera; Brachycera;
Muscomorpha; Ephydroidea; Drosophilidae; Drosophila.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              SEQUENCE
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                                                                                                                                                                                                                                                                                                                                                                                  [CE1_DROME
                                                                                                                                                                                                                                                                                                                                                                                                                                                 302
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Local (
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      97
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    McCall K., Steller H.;
    a Drosophila cell death protease essential for development.";
    nce 275:536-540(1997).

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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          EADFLFAYSTVPGYYSWRSPGRGSWFVQALCSILEEHGKELEIMQILTRVNDRVARHFES
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                SKKKKNVTMRSIKTTRDRVPTYQYNMNFEKLGKCIIINNKNFDKVTGMGVRNGTDKDAEA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   TPIKDLTAHFRGDRCKTLLEKPKLFFIQACRGTELDDAIQAD.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           LTRVLKQLDFEVTVYKDCRYKDILRTIEYAASQNHSDSDCILVAILSHGEMGYIYAKDTQ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         LFKCFRSLGFDVIVYNDCSCAKMQDLLKKASEEDHTNAACFACILLSHGEENVIYGKDGV 156
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          SSYRKNVA----KMVTDR-HAAEYNMRHKNRGMALIFNHEHFE-VPTLKSRAGTNVDCEN 121
                                                                                                                                                                                                                                                                                                                                                                                                                                                                     -QSDDPHFHEKKQIPCVVSMLTKELYFS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            HADFLIAYSTVPGFYSWRNTTRGSWFMQSLCAELAANGKRLDILTLLTFVCQRVAVDFES
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            YKLDNIWSFFTANHCPSLAGKPKLFFIQACQGDRLDGGVTMQRSQTETDGDSSMSYKIPV
                                                                                                           McCall K., Steller 277:167-167(1997).
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PS50207;
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                                                                                                                                                                                                                                                                                                                                                                                   STANDARD;
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217
230
339
169
211
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265
37363
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CASPASE_P10;
CASPASE_P20;
                                                                                                                                                                                               PubMed=8999799;
                                                                                                                                                                                                                      AND SEQUENCE OF
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       33.4%;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      CASPASE SUBUNIT P21 (
BY SIMILARITY:
CASPASE SUBUNIT P12 (
BY SIMILARITY:
BY SIMILARITY:
BY SIMILARITY:
A -> S (IN REF: 1).
S -> T (IN REF: 1).
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Score 539;
Pred. No. 2
                                                                                                                                                                                                                                                                                                                                                                                   PRT;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                       302
                                                                                                                                                                                                                                                                                                                                                                                   323
                                                                                                                                                                                                                                                                                                                                  update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       DB 1;
.8e-39;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            98;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   -SGPINDTDANPRYKIPV
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Length
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                        S.N.,
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           241
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SMART; SM00115; CASC; 1.
PROSITE; PS01122; CASPASE_HIS; 1.
PROSITE; PS01121; CASPASE_HIS; 1.
PROSITE; PS01207; CASPASE_P10; 1.
PROSITE; PS50207; CASPASE_P20; 1.
PROSITE; PS50208; CASPASE_P20; 1.
Hydrolase; Thiol protease; Zymogen; Ar

Pfam; PF00655; ICE_p10; 1. Pfam; PF00656; ICE_p20; 1. InterPro; IPR002398; ICE. InterPro; IPR002138; ICE_p10 InterPro; IPR001309; ICE_p20

FlyBase; FBgn0010501; MEROPS; C14.016;

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RA Fosler C., Garg N.S., Gelbart W.M., Glasser K.,
RA Glodek A., Gong F., Gorrell J.H., Gu Z., Guan P., Harris M.,
RA Harris N.L., Harvey D., Heiman T.J., Hernandez J.R., Houck J.,
RA Harris N.L., Harvey D., Heiman T.J., Wei M.-H., Ibegwam C.,
RA Hostin D., Houston K.A., Howland T.J., Wei M.-H., Ibegwam C.,
RA Kimmel B.E., Kodira C.D., Kraft C., Kravitz S., Kulp D., Lai Z.,
RA Kimmel B.E., Kodira C.D., Kraft C., Kravitz S., Kulp D., Lai Z.,
RA Lasko P., Lei Y., Levitsky A.A., Li J., Li Z., Liang Y., Lin X.,
RA Merkulov G., Milshina N.V., Mobarry C., Morris J., Moshrefi A.,
RA Merkulov G., Milshina N.V., Mobarry C., Morris J., Moshrefi A.,
RA Melson D.R., Nelson K.A., Nixon K., Nusskern D.R., Pacleb J.M.,
RA Palazzolo M., Pittman G.S., Pan S., Pollard J., Pacleb J.M., Resee M.G.,
RA Reinert K., Remington K., Saunders R.D.C., Scheeler F., Shen H.,
RA Spier E., Spradling A.C., Stapleton M., Stupski M.P., Smith T.,
RA Spier E., Spradling A.C., Stapleton M., Stupski M.P., Smith T.,
RA Wang Z.-Y., Wassarman D.A., Weinstock G.M., Weissenbach J.,
RA Willams S.M., Woodage T., Worley K.C., Wu D., Yang S., Yao Q.A.,
RA Willams S.M., Woodage T., Weinstock G.M., Weissenbach J.,
RA Zheng X.H., Zhong F.N., Zhong W., Zhou X., Zhu X., Smith H.O.,
RA Zheng X.H., Zhong F.N., Zhong W., Zhou X., Zhu X., Smith H.O.,
RA Zheng X.H., Zhong F.N., Rubin G.M., Venter J.C.;
"The genome sequence of Drosophila melanogaster.";
Science 287:2185-2195(2000).
C. PROTEOLYTICALLY CLEAVES POLY(ADP-RIBOSE) POLYMERASE (PARP). LOSS OF ZYGOTIC DCP-1 FUNCTION CAUSES LARVAL LETHALITY AND MELANOTIC
C. THMORS.
                                                                                                                                                                                                                                                                                   This SWISS-PROT entry is copyright. It is produced through between the Swiss Institute of Bioinformatics and the EN the European Bioinformatics Institute. There are no restruse by non-profit institutions as long as its content modified and this statement is not removed. Usage by and entities requires a license agreement (See http://www.isb-s
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EMBL; AE003461;
HSSP; P42574; 1
                                                     EMBL; AF001464; AAB58237.1; -. EMBL; AE003461; AAF47027.1; -.
                                                                                                                                                                                                                             entities requires a license agreement (some send an email to license@isb-sib.ch).
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w R.M., Basu A., Baxendale J., Bayraktaroglu L., E
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Fleischmann
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O1-NOV-1997 (Rel. 35, Created)
O1-NOV-1997 (Rel. 35, Last sequence update)
15-JUN-2002 (Rel. 41, Last annotation update)
Caspase-6 precursor (EC 3.4.22.-) (Apoptotic CASP6.
                                  This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation -
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van Loo G., Molemans F., Schotte
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                                                                                                                                                                                                                                                                Fiers W.
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            European Bioinformatics Institute. The by non-profit institutions as long
                                                                                                                                                                     FUNCTION: INVOLVED IN THE ACTIVATION CASCADE OF CASPASES RESPONSIBLE FOR APOPTOSIS EXECUTION. CLEAVES POLY(ADD-RIBOSE) POLYMERASE IN VITRO, AS WELL AS LAMINS. OVEREXPRESSION PROMOTES PROGRAMMED CELL DEATH (BY SIMILARITY).
SUBUNIT: HETERODIMER OF A 18 kDa (P18) AND A 11 kDa (P11) SUBUNITED.
                                                                   SUBUNITS (BY SIMILARITY).
SIMILARITY: BELONGS TO PEPTIDASE FAMILY C14.
                                                                                                                                    SUBCELLULAR LOCATION: Cytoplasmic.
TISSUE SPECIFICITY: HIGHLY EXPRESSED IN LUNG,
                                                                                                                                                             (BY
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ICE6_HUMAN
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Best Local :
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Pfam; PF00656; ICE_P20; 1.

PRINTS; PR00376; ILIBCENZYME.

SMART; SM00115; CASC; 1.

PROSITE; PS01122; CASPASE_CYS; 1.

PROSITE; PS01121; CASPASE_HIS; 1.

PROSITE; PS01171; CASPASE_P10; 1.

PROSITE; PS50208; CASPASE_P20; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ACT_SITE
ACT_SITE
SEQUENCE
                                                                                                                                                     01-OCT 1996 (Rel. 34, Created)
01-OCT-1996 (Rel. 34, Last sequence update)
15-JUN-2002 (Rel. 41, Last annotation update)
Caspase-6 precursor (EC 3.4.22.-) (Apoptotic
                                                            TISSUE=T-cell;
                                                                                                           Eukaryota; Metazoa;
Mammalia; Eutheria;
                                                                                                                                                CASP6 OR MCH2
                                                                                                                                                                                                            ICE6_HUMAN P55212;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 PROPEP
                     MEDLINE=95316841; PubMed=7796396; Pernandes-Alnemri T., Litwack G., Alr
Mch2, a new member of the apoptotic
                                  MEDLINE-95316841;
Fernandes-Alnemri
                                                                       SEQUENCE FROM N.A.
            family
                                                                                                NCBI_TaxID=9606
                                                                                                                                    Homo sapiens (Human)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       CHAIN
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InterPro; IPR001309;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             HSSP; P42574;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       EMBL; Y13087; CAA73529.1;
                                                                                                                                                                                                                                                                                                                                                          227
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       InterPro; IPR002398;
                                                                                                                                                                                                                                                                                                                                                                                                                                                          116
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       56 PTYQYNMNFEKLGKCIIINNKNFDKVTGMGVRNGTDKDAEALFKCFRSLGFDVIVYNDCS 115
                                                                                                                                                                                                                                                                                                                                                                                               EKPKLFFIQACRGTELDDAI------
                                                                                                                                                                                                                                                                                   QVPCFASMLTKKLHF
                                                                                                                                                                                                                                                                                                                                                                                                                                               CAKMQDLLKKASEEDHTNAACFACILLSHGEENVIYGKDGVTPIKDLTAHFRGDRCKTLL 175
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 PAEQYKMDHKRRGVALIFNHERFFWHLTLPERRGTNADRDNLTRRFSDLGFEVKCFNDLR 75
                                                                                                                                                                                                                                                                                                         QIPCVVSMLTKELYF
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99; Conserv
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6 162

163 176

177 276

104 104
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276
55:2737-2742(1995).
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                                                                                                                                                                                                                         STANDARD;
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                                                                                                             Chordata;
Primates;
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38.8%;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ; Apoptosis; Zymogen.
BY SIMILARITY.
CASPASE-6 SUBUNIT F
BY SIMILARITY.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                43;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Score 483.5; DB 1;
Pred. No. 1.3e-34;
3; Mismatches 104;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        BY SIMILARITY.
BY SIMILARITY.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     CASPASE-6 SUBUNIT P11
                                                                                                           Craniata; Vertebrata; l
Catarrhini; Hominidae;
                                                                                                                                                                                                                         PRT;
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                                    Alnemri E.S.
                        Ced-3/Ice
                                                                                                                                                                                                                         293
                                                                                                                                                                                                                         B
                                                                                                                                                          protease Mch-2).
                      cysteine
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                                                                                                                        Euteleostomi;
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                      protease
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Best Local
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InterPro; IPR002138; ICE_P10.
InterPro; IPR001309; ICE_P20.
Pfam; PF00655; ICE_P10; 1.
Pfam; PF00656; ICE_P20; 1.
PRINTS; PR00376; IL1BOENZYME.
SMART; SM00115; CASC; 1.
                                                                                                                                                                                               ACT_SITE
ACT_SITE
VARSPLIC
SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    EMBL;
                                                                                                                                                                                                                                                                                                                PROSITE; PS0112; CASPASE_CYS;
PROSITE; PS01121; CASPASE_HIS;
PROSITE; PS50207; CASPASE_P10;
PROSITE; PS50208; CASPASE_P20;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  This
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              the lamin-cleaving enzyme Mch2alpha are substrates for the mediator CP932.";
J. Biol. Chem. 271:27099-27106(1996).
-i- FUNCTION: INVOLVED IN THE ACTIVATION CASCADE OF CASPASE RESPONSIBLE FOR APOPTOSIS EXECUTION. CLEAVES POLY(ADP-R POLYMERASE IN VITRO, AS WELL AS LAMINS. OVEREXPRESSION PROGRAMMED CELL DEATH.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              TISSUE-Lymphocytes;
MEDLINE-97059171; PubMed-
Srinivasula S.M., Fernand
Armstrong R.C., Wang L.,
                                                                                                                                                                                                                                                                  PROPEP
                                                                                                                                                                                                                                                                                            PROPEP
                                                                                                                                                                                                                                                                                                                                                                                                                                                              MIM; 601532;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Genew;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     MEROPS;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     between
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                176
                                                                  116
                                         93
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  SUBUNIT: HETERODIMER OF A 18 kDa (P18) AND A 11 kDa SUBCELLULAR LOCATION: CYTOPLASMIC.
ALTERNATIVE PRODUCTS: 2 ISOFORMS; ALPHA (SHOWN HERE ARE PRODUCED BY ALTERNATIVE SPLICING. THE BETA ISOF SEEM TO HAVE PROTEOLYTIC ACTIVITY.

PTM: CLEAVAGES BY CPP32, CASPASE-8 OR -10 GENERATE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         SIMILARITY: BELONGS TO PEPTIDASE FAMILY C14
EKPKLFFIQACRGTE-
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  SWISS-PROT entry is copy
een the Swiss Institute
                                                                                                                 PTYQYNMNFEKLGKCIIINNKNFDKVTGMGVRNGTDKDAEALFKCFRSLGFDVIVYNDCS 115
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Ced-3/interleukin lbeta converting
                                       AEELLLKIHEVSTVSHADADCFVCVFLSHGEGNHIYAYDAKIEIQTLTGLFKGDKCHSLV
                                                               CAKMQDLLKKASEEDHTNAACFACILLSHGEENVIYGKDGVTPIKDLTAHFRGDRCKTLL 175
                                                                                         PAEKYKMDHRRRGIALIFNHERFFWHLTLPERRRTCADRDNLTRRFSDLGFEVKCFNDLK
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 U20536; AAC50168.1;
U20537; AAC50169.1;
P42574; 1PAU.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                       HGNC:1507; CASP6
                                                                                                                                            Similarity 37.9
97; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        C14.005;
                                                                                                                                                                                                  293 AA;
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180
194
194
121
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                                                                                                                                                                                                                                                                                                     protease;
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Fernandes-Alnemri T.,
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179
193
293
121
163
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                                                                                                                                                         28.9%;
37.9%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 copyright. It is produced through tute of Bioinformatics and the EM
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                                                                                                                                                                                                  ₹.
                                                                                                                                             42;
                                                                                                                                                                                                                                                                                                     Apoptosis;
                                                                                                                                                                                                        CASPASE-6 SUBUN
BY SIMILARITY.
BY SIMILARITY.
MISSING (IN ISO
                                                                                                                                          Score 466; DB 1;
Pred. No. 4.7e-33;
2; Mismatches 107
                                                                                                                                                                                                                                                                            CASPASE-6 SUBUNIT
 -LDDAIQADSGPINDTDANPRYKIPVEADFLFAYST
                                                                                                                                                                                              BD9204E23CE1F670 CRC64;
                                                                                                                                                                                                                                                                                                   Zymogen; Alternative splicing.
                                                                                                                                                                                                                                                  SUBUNIT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  There are no restrictions
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Tomaselli K.J.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             enzyme-like hon substrates for
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Zangrilli J., Robertson
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                                                                                                                                             107;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             SHOWN HERE) AND
BETA ISOFORM DO
                                                                                                                                                                                                                                                  P11
                                                                                                                                                                                                                                                                            P18
                                                                                                                                                                    Length
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POLY(ADP-RIBOSE)
                                                                                                                                             Indels
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                                                                                                                                                                       293;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           the apoptotic
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Litwack
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                                                                                                                                             10;
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             225
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LCEB_HUMAN STANDARD; PRT; 479 AA.

AC Q14790; Q14791; Q14792; Q14793; Q14794; Q14795; Q14796; Q15780;

AC Q15806; Q9UQ81; Q14676;

DT Q1-NOV-1997 (Rel. 35, Created)

DT Q1-NOV-1997 (Rel. 35, Last sequence update)

DT 15-JUN-2002 (Rel. 41, Last annotation update)

DE Caspase-8 precursor (EC 3.4.22.-) (ICE-like apoptotic protease 5)

DE (MORT1-associated CED-3 homolog) (MACH) (FADD-homologous ICE/CED-3-

DE like protease) (FADD-like ICE) (FLICE) (Apoptotic cysteine protease)

C (Apoptotic protease MCH-5) (CAP4).
  ACD DECEMBER OF THE PROPERTY O
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ICE8_HUMAN
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                                                                                                                                                                                                                                                                                            SEQUENCE FROM N.A.
MEDLINE-99132295; PubMed-99
Grenet J., Teitz T., Wei T.
"Structure and chromosome 1:
Gene 226:225-232(1999).
                                                                  Srinivasula S.M., Ahmad M., Ottilie S., Bul
Fernandes-Alnemri T., Croce C.M., Litwack G
Armstrong R.C., Alnemri E.S.;
"FLAME-1, a novel FADD-like anti-apoptotic
Fas/TNFRI-induced apoptosis.";
J. Biol. Chem. 272:18542-18545(1997).
                                                                                                                                                                                                                                                                                                                                                                                                                         apoptotic cysteine protease containing two FADD-like domains. Proc. Natl. Acad. Sci. U.S.A. 93:7464-7469(1996).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Muzio M., Chinnaiyan A.M., Kischkel F.C., O'Rourke K., Sh
Ni J., Scaffidi C., Bretz J.D., Zhang M., Gentz R., Mann
Krammer P.H., Peter M.E., Dixit V.M.;
"FLICE, a novel FADD-homologous ICE/CED-3-like protease,
to the CD95 (Fas/APO-1) death-inducing signaling complex.
Cell 85:817-827(1996).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                MEDLINE=96353838; PubMed=8755496; Fernandes-Alnemri T., Armstrong R. Wang L., Bullrich F., Fritz L.C., Litwack G., Alnemri E.S.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               SEQUENCE FROM N.A., AND ALTERNATIVE TISSUE-Thymus, and B-cell; MEDLINE-96279826; PubMed-8681376;
                                                                                                                                                                                             MEDLINE-97373543;
Srinivasula S.M.,
                                                                                                                                                                                                                            SEQUENCE FROM N.A. (ISOFORM 2-ALPHA).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Boldin M.P., Goncharov T.M., Goltsev Y.V., Wallach D "Involvement of MACH, a novel MORTI/FADD-interacting Fas/APO-1- and TWF receptor-induced cell death.";
PARTIAL SEQUENCE,
MEDLINE-97121412;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         TISSUE-T-cel
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                SEQUENCE FROM
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Eukaryota; Metazoa; Chordata; Craniata; Vo
Mammalia; Eutheria; Primates; Catarrhini;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    SEQUENCE FROM N.A.,
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T., Wei T., Valentine
romosome localization
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  AND PROCESSING PubMed=8962078;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Blanchard H., Kodandapani L., Mittl P.R.E., Wu J.C., Tomaselli K.J., Gruetter M.G.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Muzio M., Salvesen G.S., Dixit V.M.; *FLICE induced apoptosis in a cell-free
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            "Molecular ordering of the Fas-apoptotic pathway: the Fas/APO-1 protease Mch5 is a CrmA-inhibitable protease that activates multiple Ced-3/ICE-like cysteine proteases.";
Proc. Natl. Acad. Sci. U.S.A. 93:14486-14491(1996).
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Medema J.P., Scaffidi
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Alnemri E.S.;
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PTM: GENERATION OF THE SUBUNITS REQUIRES ASSOCIATION WITH TO PICTURE.

DISC, WHEREAS ADDITIONAL PROCESSING IS LIKELY DUE TO THE AUTOCATALYTIC ACTIVITY OF THE ACTIVATED PROTEASE. GRANZYME CASPASE-10 CAN BE INVOLVED IN THESE PROCESSING EVENTS.

SIMILARITY: BELONGS TO PETIDASE FAMILY C14.

SIMILARITY: CONTAINS 2 DEATH EFFECTOR DOMAINS (DED).
                                                                                                                                                                       European Bioinformatics Institute.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                      RECRUITS IT TO EITHER RECEPTORS. THE RESULTING AGGREGATE CALLED THE DEATH-INDUCING SIGNALING COMPLEX (DISC) PERFORMS FLICE/MACH PROTEOLYTIC ACTIVATION. THE ACTIVE DIMERIC ENZYME IS THEN LIBERATED FROM THE DISC AND FREE TO ACTIVATE DOWNSTREAM APOPTOTIC PROTEASES. PROTEOLYTIC FRACMENTS OF THE N-TERMINAL PROPEPTIDE (TERMED CAP3, CAP5 AND CAP6) ARE LIKELY RETAINED IN THE DISC. CLEAVES AND ACTIVATES CASPASE 3, -4, -6, -7, -9, AND -10. MAY PARTICIPATE IN THE GRANZYME B APOPTOTIC PATHWAYS. PROTEOLYTICALLY CLEAVES POLY(ADP-RIBOSE) POLYMERASE (PARP). HYDROLYZES THE SMALL-MOLECULE SUBSTRATE, AC- ASP-GLU-VAL-ASP-|-AMC. LIKELY TARGET FOR THE COMPON VIRUS CRMA DEATH INHIBITORY PROTEIN.
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BETA; ARE PRODUCED BY ALTERNATIVE SPLICING
TISSUE SPECIFICITY: ALPHA 1 AND BETA 1 ISOFORMS ARE
WIDE VARIETY OF TISSUES. HIGHEST EXPRESSION IN PERIP
LEUKOCYTES, SPLEEN, THYMUS, AND LIVER. BARELY DETECT
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sen the Swiss Institute of Bioinformatics and the EN
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                                                                                                                    requires a license agreement (See http://www.isb-sib
                                                                                                                                      and this statement is not removed
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InterPro; IPR001309; ICE_p20
Pfam; PF00655; ICE_p10; 1.
Pfam; PF00656; ICE_p20; 1.
Pfam; PF01335; DED; 2.
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AF102141; AAD24962.1;
AF102142; AAD24962.1;
AF102143; AAD24962.1;
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PS01121; CASPASE_HIS;
PS50207; CASPASE_P10;
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AAD24962.
                                                                                                                  SLEGSPDEFSNGEELCGVMTISDSPREQDSESQTLDKV
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                protease;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     CASP8
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55391
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235
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374
                                                                                                                                                                                                     26.4%;
                                                                                 DKVTGMGVRNGTDKDAEALFKCFRSLGFDVIVYNDCSCAK
                                                                                                                                                                                                                                                        MW;
                                                                                                                                                                                     49;
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                                                                                                                                                                                                                                                                 BETA).

D -> H (IN REF. 3
E -> D (IN REF. 4
A -> P (IN REF. 2
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Pred. No. 2.
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MISSING (IN ISOFORM 1 BETA).
                                                                                                                                                                                                                                                                                                                                                                       ALTTTFEE
                                                                                                                                                                                                                                                                                                                                                                                                                                                          GEELCGVMTISDSPREQDSESQTLDKVYQMKSKPRGY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        MISSING (IN ISOFORM 2 ALPHA, ISOFORM ALPHA AND ISOFORM 4 BETA).

ERSSSLEGSPDEFSNGEELCGVMTISDSPREQDSESO
                                                                                                                                                                                                                                                                                                                                                                                                                                         DFGQSLPNEKQTSGILSDHQQSQFCKSTGESAQTSQH
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                                                                                                                                                                                                                                                                                                                                                                                                                           ISOFORM
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                                                                                                                                                                                     Mismatches
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                          (IN ISOFORM 3 ALPHA)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Zymogen; Alternative splicing;
                                                                                                                                                                                                                                                                                                                                                                                                                         BETA)
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                                                                                                                                                                                                   .7e-29;
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                                                                                                                  -YQMKSK
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                                                                                                                                                                                Gaps
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protease Mch5 is
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01-NOV-1997 (Rel. 35, Created)
01-NOV-1997 (Rel. 35, Last squence update)
15-JUN-2002 (Rel. 41, Last annotation update)
Caspase-10 precursor (EC 3.4.22.-) (ICE-like apoptotic protease
(Apoptotic protease Mch-4) (FAS-associated DEATH domain protein
                                                                                                                                                                                                                                                                                                                                                                                                                                                                            TISSUE-Thymus, and Spleen;
MEDLINE-99214592; PubMed=10187817;
Ng P.W., Porter A.G., Janicke R.U.
                                                                                   Srinivasula
                                                                                                       PARTIAL SEQUENCE, MEDLINE-97121412;
                                                                                                                                                                                           "Cloning and characterization of three novel genes, ALS2CR1, ALS2CR2, and ALS2CR3, in the juvenile amyotrophic lateral sclerosis (ALS2) critical region at chromosome 2q33-q34: candidate genes for ALS2.";
                                                                                                                                                                                                                                                                     Hadano S., Yanagisawa Y., Skaug J.,
Martindale D., Koop B.F., Scherer S.
Ikeda J.-E., Hayden M.R.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               enzyme
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       MEDLINE=97197836; PUBMED=9045886; Vincenz C., Dixit V.M.; "Fas-associated"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                "In vitro activation of CPP32 and Mch3 by Mch4, a novel human apoptotic cysteine protease containing two FADD-like domains."; Proc. Natl. Acad. Sci. U.S.A. 93:7464-7469(1996).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Homo sapiens (Human).
Eukaryota; Metazoa; Chordata;
Mammalia; Eutheria; Primates;
                                                              Alnemri E.S.
                                                                                                                                                                                                                                                                                                                                      SEQUENCE FROM N.A. (ISOFORM A), MEDLINE=21100893; PubMed=11161814;
                                                                                                                                                                                                                                                                                                                                                                                                                                          "Molecular cloning and characterization
isoforms of caspase-10.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Fernandes-Alnemri
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                MEDLINE-96353838;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           SEQUENCE FROM N.A. (ISOFORM
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  CASP10 OR MCH4.
                                                                                                                                                                                                                                                                                                                                                                                                                                      isoforms of caspase-10
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          NNCVSYRNPAEGTWYIQSLCQSLRERCPRGDDILTILTEVN----YEVSNKDDKKNMG
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        G., Alnemri E.S.
                                                                                                                                                                                                                                                                                                                                                                                                                  Chem.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  (FLICE2), an ICE/Ced-3 homologue, p55-mediated death signaling.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    FROM N.A.
                                                                                                                                                                            71:200-213(2001).
         ordering of the Fas-apoptotic pathway: the Fas/APO-1 ch5 is a CrmA-inhibitable protease that activates multiple
                                                                                 S.M.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               272:6578-6583(1997).
                                                                                                                                                                                                                                                                                                                                                                                                           274:10301-10308(1999)..
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                death domain protein interleukin-1beta-converting
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         PubMed=8755496;
IT., Armstrong R.O.
h F., Fritz L.C.,
                                                                                 Ahmad M.,
                                                                                                         PubMed=8962078;
                                                                                                                               AND PROCESSING.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 (ISOFORMS B AND
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Janicke R.U.;
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                                                                            Fernandes-Alnemri T.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         A).
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Trapani J.A.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 C
                                                                                                                                                                                                                                                                                 Fichter K., Nasir J.,
.W., Nicholson D.W., Rouleau G.A.,
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Tomaselli K.J.,
                                                                               Litwack
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; Homo.
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RT Ced-3/ICE-like cysteine proteases.";

R1 Proc. Natl. Acad. Sci. U.S.A. 93:14486-14491(1996).

R2 -!- FUNCTION: INVOLVED IN THE ACTIVATION CASCADE OF CASPASES

RESPONSIBLE FOR APOPTOSIS EXECUTION. RECRUITED TO BOTH FAS- AND

ROTHE GRANZYME B APOPTOSIS EXECUTION. RECRUITED TO BOTH FAS- AND

ROTHER-1 RECEPTORS IN A FADD DEPENDENT MANNER. MAY PARTICIPATE IN

CONTROL OF THE GRANZYME B APOPTOTIC PARTHWAYS. CLEAVES AND ACTIVATES CASPASE-

CONTROL OF THE SMALL- MOLECULE

SUBSTRATES, TYR-VAL-ALA-ASP-|-AMC AND ASP-GLU-VAL-ASP-|-AMC.

CONTROL OF THETERODIMER OF A 23/17 AND ASP-GLU-VAL-ASP-|-AMC.

CONTROL OF THE STATE PRODUCTS: 3 ISOFORMS; AND COLON HERE), B/10-B AND

CONTROL OF THE STATE PRODUCED BY ALTERNATIVE SPLICING

CONTROL OF THE STAND AND ALTERNATIVE SPLICING.

CONTROL OF THE STAND AND AUTOCATALYTIC ACTIVITY GENERATE
                                                                                                                                                                                                                                                                                                                                                                                                                                           PROSITE; PS01122; CASPASE_US;
PROSITE; PS01121; CASPASE_HIS;
PROSITE: PS50207; CASPASE_P10;
PROSITE; PS50208; CASPASE_P20;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          SMART; SM00115; CASC; SMART; SM00031; DED;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       SIMILARITY: BELONGS TO PEPTIDASE FAMILY C14.
SIMILARITY: CONTAINS 2 DEATH EFFECTOR DOMAINS (DED).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    European Bioinformatics Institute.
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THE TWO ACTIVE SUBUNITS.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        SWISS-PROT entry is copyright. It is produced through a ceen the Swiss Institute of Bioinformatics and the EMBL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             PF01335:
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                                                                                                                                                                                                                                                                                                                                                                                                                    PS50208;
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; IPR002138; ICE_p10.
; IPR003309; ICE_p20.
00655; ICE_p10; 1.
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                                                                                                                                                                                                                                                                                                                                                                                          Thiol
                                                                                                            splicing.

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401 401

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473 521
                            241
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DED; 2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   1QDU.
                                                                                                                                                                                                                                                                                                                                                                                          protease;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                IL1BCENZYME
                                                                                                                                                                                                                                                                                                                                                                                                                       DED;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            DED.
                                                                                                                                                                                                                                                                                                                                                                                        Apoptosis;
                                                                                                                                                                                                                                                  CASPASE-10
CASPASE-10
DED 1.
MLKFLEKTMEIRGRKRTVWGAKQISATSLPTAISAQTPRPP
MRRWSSYS -> HEDILSILTAVNDDVSRRVDXGGTKKQMP
QPAFTLRKKLVFPVPLDALSI (IN ISOFORM B).
GNRATNGAPSLVSRGMCGASANTLNSETSTKRA -> EGSC
VQDESEPQRPLCHCQQPQLYLPEGQTRNP (IN ISOFORM
                                                                                                                                   BY SIMILARITY.
BY SIMILARITY.
MISSING (IN SHORT ISOFORM)
                                                                                                                                                                                                                                                                                                                                                                                     Zymogen;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              There are no
                                                                                                                                                                                                                                                                              SUBUNIT P23/17.
                                                                                                                                                                                                                                                                                                                                                                                     Repeat;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              restrictions
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                a collaboration
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Sear Job	Db Qy	Db Oy	Оy	Qy Db	Qy Db	Dp 65	Be Ma	FT FT FT SQ
Search completed: December 2, 2002, 12:56:29 Job time : 11.4483 secs	287 QIPCVVSMLTKEL 299 : :: : 469 LVPRMLKELEKTM 481	227 PGYYSWRSPGRGSWFVQALCSILEEHGKELEIMQILTRVNDRVARHFESQSDDPHFHEKK 286	169 DRCKTLLEKPKLFFIQACRGTELDDAIQADSGPINDTDANPRYKIPVEADFLFAYSTV 226 	111 YNDCSCAKMODLLKKAS-EEDHTNAACFÁCILLSHGEENVIYGKD-GVTPIKDLTAHFRG 168 	51 TRDRVPTYQYNMNFEKLGKCIIINNKNFDKVTGMGVRNGTDKDAEALFKCFRSLGFDVIV 110 :	11 QGVEDSANEDSVDAKPDRSSFVPSLFSKKKKNYTMRSIKT 50	Query Match 24.5%; Score 395; DB 1; Length 521; Best Local Similarity 30.4%; Pred. No. 1.3e-26; Matches 95; Conservative 55; Mismatches 99; Indels 64; Gaps 9;	VARSPLIC 274 521 MISSING (IN ISOFORM C). CONFLICT 68 68 E -> G (IN REF. 2). CONFLICT 268 268 T -> A (IN REF. 3). CONFLICT 410 410 V -> I (IN REF. 3). SEQUENCE 521 AA; 58950 MW; 840348AE602B8243 CRC64;

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Result
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Database :
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Minimum DB
Maximum DB
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Post-processing: Minimum Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Minimum
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Total number of hits satisfying chosen parameters:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Scoring table:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Perfect score:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Title
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Run on:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         OM protein - protein search, using sw model
                                                                                                                                                                                                                                   ŏ
                                                                                                                                                                                                                                                                                              Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.
                                          720.5
719
623.5
512.5
510.5
493.5
483.5
                                                                                                                                                   1025
744.5
743
721
                                                                                                                                                                                                                                   Score
    473
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seq
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        length: 2000000000
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  44.6
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31.0
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29.8
29.4
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           671580 segs, 206047115 residues
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Gapop 10.0 , Gapext 0.5
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          1 MADDQGCIEEQGVEDSANED.....EKKQIPCVVSMLTKELYFSQ 303
                                                                                                                                                   44
                                                                                                                                                                 46
                                                                                                                                                                                                                                                                                                                                                                                                                                                      10:
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1613
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                                                                                                                                                                             46
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         SPTREMBL_21:*
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               GenCore version 5.1.3 Copyright (c) 1993 - 2002 Compugen Ltd.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                  sp_phage:*
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          sp_mammal:*
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  sp_fungi:*
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              sp_bacteria:*
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            sp_archea:*
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 sp_organelle:*
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        sp_invertebrate:*
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     sp_human:*
                                                                                                                                                                                                                                                                                                                                                                                sp_unclassified:*
sp_rvirus:*
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                                                                                                                                                                                                                                                                                                                                                        sp_archeap:*
                                                                                                                                                                                                                                                                                                                                                                    sp_bacteriap:*
                                                                                                                                                                                                                                                                                                                                                                                                           sp_vertebrate:*
                                                                                                                                                                                                                                                                                                                                                                                                                           sp_virus:*
                                                                                                                                                                                                                                                                                                                                                                                                                                         sp_rodent:*
                                                                                                                                                                                                                                                                                                                                                                                                                                                   sp_plant:*
                                                                                                                                                                                                                                  Length DB
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            2, 2002, 12:54:49 ; Search time 28.7328 Seconds
                                                     Q9I8S9
077623
 Q9BQE7
Q9D089
                                                                                                                     Q96AN1
Q95ND5
Q96KP2
                                                                                                                                                                                                                                ID
                                                                                             Q9QWI4
093415
                                                                                                                                                              Q98UI8
093417
                                                                                                                                                                                       088550
Q9IB65
                                                                                                                                                                                                                                                                        SUMMARIES
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                (without alignments)
2172.860 Million cell updates/sec
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               671580
                        093415 gallus gall
091b66 xenopus lae
091889 oncorhynchu
077623 ovis aries
099m47 mus musculu
035397 rattus norv
                                                                                                                 Q96an1 homo sapien
Q95nd5 sus scrofa
Q96kp2 homo sapien
                                                                                                                                                           088550 rattus norv
Q9ib65 xenopus lae
Q98ui8 brachydanio
Q93417 gallus gall
Q9bqe7 homo sapien
Q9d089 mus musculu
                                                                                                                                                                                                                               Description
                                                                                                        Q9qwi4 mus musculu
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252	255	255.5	275.5	284	284	305	305	. 305	309	314.5	317	356.5	362	364.5	371.5	372.5	377.5	396	411.5	414.5	423.5	425.5	443	444.5	446	446	446.5	447.5
15.6	15.8	•			•	٠	18.9	•			•		22.4	22.6	23.0	23.1	23.4	24.6	25.5	25.7	26.3	26.4	27.5	27.6	27.7	27.7	27.7	27.7
339	347	450	393	536	268	826	452	263	423	417	435	416	500	454	520	403	454	476	326	399	496	538	482	479	308	308	482	480
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Q8TDI3	Q9GV89	Q9XYF4	Q9R0S9	018203	Q9TZP6	Q9Y055	055194	Q9TZP5	Q9IB67	Q9Y1U6	Q9BUP7	Q9вQ62	Q9IB64	Q9JНК1	Q9IB62	Q90WU0	Q9R0T0	Q918J3	Q9GV88	Q9IB63	Q9C0K4	Q8TDI5	Q9JНX4	80AM80	Q9VET9	Q9NHF9	Q90WU1	089110
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Q8tdi3	Q9qv89	Q9xyf4	Q9r0s	018203	Q9tzp6	09y05	055194	09tzp	091b67	Q9y1u6	09bup	09bq6	091b64	Q9†hk1	Q91b62	090wu0	Q9r0t0	Q918j3	Q9qv8	091b63	Q9c0k4	Q8tdi5	Q9jhx4	Q8wyq8	. Q9vet9	Q9nhf9	Q90wu1	089110

ALIGNMENTS

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DT RRAC OOC DT DT RRAC OOC DT DT RRAC OOC DT DD RRAC D
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   Query Match 86.9
Best Local Similarity 84.9
Matches 256; Conservative
                                                                                                                                                                                                                                                                                                                         InterPro; IPR002398; ICE.
InterPro; IPR002138; ICE_p10.
InterPro; IPR0011309; ICE_p20.
Pfam; PF00655; ICE_p10; 1.
Pfam; PF00656; ICE_p20; 1.
PRINTS; PR00376; ILBCENZYME.
SMART; SM00115; CASC; 1.
                                                                                                                                                 SEQUENCE
                                                                                                                                                                           PROSITE; PS01122; CASPASE CYS; PROSITE; PS01121; CASPASE_HIS; PROSITE; PS50207; CASPASE_P10; PROSITE; PS50208; CASPASE_P20;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         088550;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       "Rat caspase-7 sequence.";
Submitted (JUN-1998) to the EMBL/GenBank/DDBJ databases
EMBL; AF072124; AAC24011.1; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.
NCBI_TaxID=10116;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             01-NOV-1998 (TrEMBLrel. 08, 01-NOV-1998 (TrEMBLrel. 08, 01-MAR-2002 (TrEMBLrel. 20,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Caspase-7
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Forghani F., Roy S.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Rattus norvegicus (Rat)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       MEROPS; C14.004;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ISSP; P42574;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  "Rat caspase-7
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            TISSUE-SPLEEN;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          SEQUENCE FROM N.A.
                                                                                                                                             303 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         1PAU.
                                                                                                                                                 34324 MW;
                                     86.5%;
       21;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Last sequence update)
Last annotation update)
   Score 1395; DB 11;
Pred. No. 1.3e-119;
1; Mismatches 26;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               PRT;
                                                                                                                                          1.
A71728754BF199DD CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           303 AA
                                                                   Length
   Indels
                                                                          303;
   0
Gaps
0
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QΥ

1 MADDQGCIEEQGVEDSANEDSVDAKPDRSSFVPSLFSKKKKNVTMRSIKTTRDRVPTYQY 60

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Вþ
                 Qy
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                                                                      Query Match
Best Local S
Matches 196
                                                                                                             InterPro; IPR002398; ICE.
InterPro; IPR002138; ICE_p10.
InterPro; IPR002138; ICE_p20.
InterPro; IPR001309; ICE_p20.
InterPro; IPR001309; ICE_p20.
InterPro; IRR001309; ICE_p20.
I.
Pfam; PP00655; ICE_p20; I.
PRINTS; PR00376; ILIBCENZYME.
SMART; SM00115; CASC; I.
SMART; SM00115; CASC; I.
PROSITE; PS01122; CASPASE_CYS; I.
PROSITE; PS01121; CASPASE_HIS; UNKNOWN_1.
PROSITE; PS01207; CASPASE_P10; I.
PROSITE; PS0208; CASPASE_P10; I.
PROSITE; PS0208; CASPASE_P10; I.
                                                                                                                                                                                                                                                              MEDLINE-20209426; Pubmed-10744739; MEDLINE-20209426; Pubmed-10744739;
                                                                                                                                                                                                                                                                                                                                                                                          Q9IB65;
                                                                                                                                                                                                                                                                                                                                                                01-OCT-2000
01-MAR-2002
                                                                                                                                                                                                                       EMBL; AB038170;
HSSP; P42574; 1
                                                                                                                                                                                                                                                                                                                    Eukaryota; Metazoa; Chordata; Craniata; Ve
Amphibia; Batrachia; Anura; Mesobatrachia;
                                                                                                                                                                                                               MEROPS; C14.004;
                                                                                                                                                                                                                                                 family
                                                                                                                                                                                                                                                                                                            Xenopodinae; Xenopus
                                                                                                                                                                                                                                                                                                                                      Xenopus laevis (African
                                                                                                                                                                                                                                                                                                                                                XCASPASE-7
                                                                                                                                                                                                                                                        "Structure, expression and
                                                                                                                                                                                                                                                                                                                                                                                                                                               301
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                                                                                                                                                                                                                                        Biol.
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EEQGVEDSANEDSVDAKPDRSSFVPSLFSKKKKNVTMRSIKT---TRDRVPTYQYNMNFE
                                                                                                                                                                                                                                                                                                                                                                                                                                               FGR
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    RMDFEKMGKCIIINNKNFDKATGMDVRNGTDKDAEALFKCFRSLGFEVTVYNDCSCAKMQ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     al Similarity
196; Conserv
                                                                                                                                                                                                                                        Chem.
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0 (TrEMBLrel. 15,
2 (TrEMBLrel. 20,
                                                                                                        318
                                                                      Conservative
                                                                                                                                                                                                                                                                                                                                                                                                   PRELIMINARY;
                                                                                                                                                                                                                       IPAU.
                                                                                                        AA;
                                                                                                                                                                                                                              275:10484-10491(2000); BAA94748.1; -.
                                   VDAKPDRSQRFSIFSSTKKKKVEDKPPKTNNNVRIVTPAFQYKMNNG
                                                                                                        35937 MW;
                                                                               63.5%;
                                                                                                                                                                                                                                                                                                                                       clawed
                                                                     33;
                                                                                                                                                                                                                                                        function
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                                                                   Score 1025; DB 13
Pred. No. 1.1e-85;
3; Mismatches 64
                                                                                                                                                                                                                                                                                                                                                               Last sequence up
                                                                                                                                                                                                                                                                                                                                                                                                   PRT;
                                                                                                       6EBC6684AF86A128 CRC64;
                                                                                                                                                                                                                                                                                                                                     frog).
                                                                                                                                                                                                                                                        0f
                                                                                                                                                                                                                                                                                                                                                                                                   318
                                                                                                                                                                                                                                                        the
                                                                                                                                                                                                                                                                                                                             Vertebrata; Euteleostomi;
                                                                                      DB 13;
                                                                                                                                                                                                                                                                                                                                                               on update)
                                                                                                                                                                                                                                                      Xenopus laevis caspase
                                                                                                                                                                                                                                                                                                                   Pipoidea;
                                                                     64;
                                                                     Indels
                                                                                     Length
                                                                                       318;
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                                                                    Gaps
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Q98UI8
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Best Local S
Matches 147
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01-JUN-2001
01-JUN-2002
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      PROSITE; PSO1122; CASPASE_CYS;
PROSITE; PSO1121; CASPASE_HIS;
PROSITE; PSSO207; CASPASE_P10;
PROSITE; PSSO208; CASPASE_P20;
SEQUENCE 282 AA; 31522 MW;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Pfam; PF00655; ICE_p10; 1.
Pfam; PF00656; ICE_p20; 1.
PRINTS; PR00376; IL1BCENZYME.
SMART; SM00115; CASC; 1.
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InterPro; IPR002138;
InterPro; IPR001309;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Submitted (AUG-2000) to the EMBL/GenBank/DDBJ databases EMBL; AB047003; BAB32409.1; -. HSSP; P42574; 1PAU.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Brachydanio rerio (Zebrafish) (Zebra danio).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Actinopterygii; Neopterygii; Teleostei; Ostariophysi; Cypriniformes;
Cyprinidae; Danio.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      "Molecular Cloning and Gene Mammalian Caspase-3.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             SEQUENCE FROM N.A. Yabu T., Okazaki T.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Q98UI8
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                       SPGRGSWFVQALCSILEEHGKELEIMQILTRVNDRVARHFESQSDDPHFHEKKQIPCVVS
                                                                         NTMTGSWFIQSLCEMMTKYGSELELLQIMTRVNHKVALDFESTSNMPGFDAKKQIPCIVS
                                                                                                                                                              YQYNMNFEKLGKCIIINNKNFDKVTGMGVRNGTDKDAEALFKCFRSLGFDVIVYNDCSCA 117
                                                                                                                                                                                                                                                                                                                                                                          CIEEQGVEDS-ANED-----SVDAKPDRSSFVPSLFSKKKKNVTMRSIKTTRDRVPT
                                                                                                                                                                                                       KMQDLLKKASEEDHTNAACFACILLSHGEENVIYGKDGVTPIKDLTAHFRGDRCKTLLEK
                                                                                                                                                                                                                                              -RYSLNYPNIGHCIIINNKNFDRRTGMNPRNGTDVDAGNVMNVFRKLGYIVKVYNDQTVA
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147; Conserv
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(TrEMBLrel.)
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                                                                                                                                                                                                                                                                                                                                                                                                                                           46.2%;
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ICE_p20.
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nd Gene Expression
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Last sequence up
Last annotation
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Pred. No. 4.0
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272
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Best Local Similarity
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SMART; SM00115; CASC; 1.

SMART; SM00115; CASC; 1.

PROSITE; PS01121; CASPASE_CYS; 1.

PROSITE; PS01121; CASPASE_PIO; 1.

PROSITE; PS50208; CASPASE_P10; 1.

PROSITE; PS50208; CASPASE_P20; 1.

SEQUENCE 283 AA; 31675 MW; 16
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093417;
01-NOV-1998
01-NOV-1998
01-MAR-2002
  O96AN1 PRELIMINARY;
O96AN1;
O1-DEC-2001 (TrEMBLrel.
O1-DEC-2001 (TrEMBLrel.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Gallus.
NCBI_TaxID=9031;
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Gallus gallus (Chicken).
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InterPro; IPR002138; ICE_p10
InterPro; IPR001309; ICE_p20
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                                                                                                                                                                                                                                                           256
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|||||:||:
3 MLTKEMYFT 281
                                                                                                                                                                                                                                  LEIMQILTRVNDRVARHFESQSDDPHFHEKKQIPCVVSMLTKELYF 301
                                                                                                                                                                                                                                                                                                       EADSGP----DETVCQKIPVEADFLYAYSTAPGYYSWRNAAEGSWFIQSLCRMLKEHARK
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                                                                                                                                                                                                        LELMQILTRVNRRVA-EYESCSTRQDFNAKKQIPCIVSMLTKEFYF 28:
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9; AAC32602.1; -.
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Neognathae; Galliformes; Phasianidae; Phasiani
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52.48;
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08, Last sequence update)
20, Last annotation updat
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Created)
Last sequence update)
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Pred. No. 6.4e-60;
4; Mismatches 76;
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Best Local
                       SEQUENCE FROM N.A.

MEDLINE=21334413; PubMed=11440638;

Muneta Y., Shimojima Y., Mori Y.;

Muneta Y., Shimojima Y., Mori Y.;

"Porcine caspase-3: cloning and its activity during procine FK15 cells induced by porcine Fas-ligand.";

J. Interferon Cytokine Res. 21:409-415(2001).

EMBL; AB029345; BAB55544.1; -.

MEROPS; C14.003; -.
                                                                                                                                                                                                                                      01-DEC-2001
01-JUN-2002
                                                                                                                                                                                                                                                                   Q95ND5;
01-DEC-2001
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Pfam; PF00656; ICE_p20; 1.
Pfam; PF00656; ICLEp20; 1.
PRINTS; PR00376; ILLBCENZYME.
PROSITE; PS01122; CASPASE_HTS; UNKNOWN_1.
PROSITE; PS01207; CASPASE_HTS; UNKNOWN_1.
PROSITE; PS02007; CASPASE_P10; 1.
PROSITE; PS02008; CASPASE_P20; 1.
                                                                                                                                                                            Eukaryota; Metazoa;
Mammalia; Eutheria;
                                                                                                                                                                                                                         Caspase-3
                                                                                                                                                                                                                                                                                               Q95ND5
                                                                                                                                                             NCBI_TaxID=9823;
                                                                                                                                                                                                           Sus scrofa (Pig).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Hypothetical protein. SEQUENCE 277 AA; 31608 MW;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    InterPro; IPR002398; ICE.
InterPro; IPR002138; ICE_p10.
InterPro; IPR001309; ICE_p20.
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 InterPro;
                InterPro; IPR002138;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Submitted (NOV-2001) to the EMBL/GenBank/DDBJ databases EMBL; BC016926; AAH16926.1; .
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Strausberg R.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             01-MAR-2002 (TrEMBLrel. 20, La Hypothetical 31.6 kDa protein. Homo sapiens (Human).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            TISSUE-LYMPH;
                                                                                                                                                                                                                                                                                                                                                                       233
                                                                                                                                                                                                                                                                                                                                                                                                                                                             199
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        116
                                                                                                                                                                                                                                                                                                                          6
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               56
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          79
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        S
                                                                                                                                                                                                                                                                                                                                                                                  MQILTRVNDRVARHFESQSDDPHFHEKKQIPCVVSMLTKELYF
                                                                                                                                                                                                                                                                                                                                                                    MHILTRVNRKVATEFESFSFDATFHAKKQIPCIVSMLTKELYF 275
                                                                                                                                                                                                                                                                                                                                                                                                                                              SGPINDTDANPRYKIPVEADFLFAYSTVPGYYSWRSPGRGSWFVQALCSILEEHGKELEI
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     CVLLSHGEEGIIFGTNGPVDLKKITNFFRGDRCRSLTGKPKLFIIQACRGTELDCGIETD
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            HKSTGMTSRSGTDVDAANLRETERNLKYEVRNKNDLTREEIVELMRDVSKEDHSKRSSFV
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                CILLSHGEENVIYGKDGVTPIKDLTAHFRGDRCKTLLEKPKLFFIQACRGTELDDAIQAD 198
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           DKVTGMGVRNGTDKDAEALFKCFRSLGFDVIVYNDCSCAKMQDLLKKASEEDHTNAACFA 138
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ENSVDSKSIK-NLEPKIIHGSESMDSGISLDNS-----YKMDYPEMGLCIIINNKNF
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                EDSVDAKPDRSSFVPSLFSKKKKNVTMRSIKTTRDRVPTYQYNMNFEKLGKCIIINNKNF
                                                                                                                                                                                                                                                                                                                                                                                                                             SGVDDDMAC---HKIPVEADFLYAYSTAPGYYSWRNSKDGSWFIQSLCAMLKQYADKLEF
 IPR001309;
                                                                                                                                                                                                                                   1 (TrEMBLrel. 19,
1 (TrEMBLrel. 19,
2 (TrEMBLrel. 21,
                                                                                                                                                                                                                                                                                              PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Conservative
                                                                                                                                                                       Chordata; Craniata; Vertebrata; Cetartiodactyla; Suina; Suidae;
ICE_p10.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           44.7%; Score 721; DB 4; L
50.9%; Pred. No. 6.4e-58;
50. Mismatches 77;
                                                                                                                                                                                                                                Created)
Last sequence update)
Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       2F35CD3BCF7FF64A CRC64;
                                                                                                                                                                                                                                                                                              277
                                                                                                                                                                                                                                                                                              A
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                                                                                                                                                                                                                                                                                                                                                                                                 301
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Indels
                                                                                      apoptosis
                                                                                                                                                                            Euteleostomi;
Sus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             12;
                                                                                        of.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     175
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ω --

Pfam; Pfam;

PF00655;

ICE_p10;

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RESULT OPERATOR RESULT OF A COMMENT OF A COM
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Š
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Best Local S
Matches 144
Query Match
Best Local Similarity
Matches 146; Conserv
                                                                                      InterPro; IPR002398; ICE_pl0.
InterPro; IPR002138; ICE_pl0.
InterPro; IPR002138; ICE_pl0.
InterPro; IPR0031309; ICE_p20.
Pfam; PF00655; ICE_pl0; 1.
Pfam; PF00656; ICE_p20; 1.
PFRNTS; PR00376; ILIBCENZYME.
PROSITE; PS01122; CASPASE_CYS; UNKNOWN_1.
PROSITE; PS01121; CASPASE_HIS; UNKNOWN_1.
PROSITE; PS0207; CASPASE_P10; 1.
PROSITE; PS50208; CASPASE_P10; 1.
PROSITE; PS50208; CASPASE_P10; 1.
SEQUENCE 277 AA; 31642 MW; 6162767B0D2DE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Q96KP2;
                                                                                                                                                                                                                                                                                                                                 "Control of the activation of the procaspase-3 by a sequence at the N-terminus of the p17 subunit.";
Submitted (OCT-2001) to the EMBL/GenBank/DDBJ databases.
EMBL; AJ413269; CAC88866.1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           SEQUENCE Vallette
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         01-DEC-2001 (TrEMBLrel 19, 01-DEC-2001 (TrEMBLrel 19, 01-MAR-2002 (TrEMBLrel 20,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    PROSITE;
PROSITE;
PROSITE;
PROSITE;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Eukaryota; Metazoa;
Mammalia; Eutheria;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Submitted
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Homo sapiens (Human).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         CASP3
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Caspase-3
                                                                                                                                                                                                                                                                                                                                                                                                                                                         SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         NCBI_TaxID=9606;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      242
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             NPRYKIPVEADFLFAYSTVPGYYSWRSPGRGSWFVQALCSILEEHGKELEIMQILTRVND
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         GKIFGTNGPVDLKKLTSFFRGDCCRTLTGKPKLFIIQACRGTELDCGIETDSGTEDDMAC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Q---KIPVEADFLYAYSTAPGYYSWRNSKDGSWFIQSLCAALKQYVHKLELMHILTRVNR
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   NVIYGKDGYTPIKDLTAHFRGDRCKTLLEKPKLFFIQACRGTELDDAIQADSGPINDTDA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           NGTDKDAEALFKCFRSLGFDVIVYNDCSCAKMQDLLKKASEEDHTNAACFACILLSHGEE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          KTSVDSKSIKTLETKILHGSKSMDSGISLDVSYKMDYPEMGLCIIINNKNFDKNTGMACR
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      KKNVTMRSIKTTRDRV-------PTYQYNMNFEKLGKCIIINNKNFDKVTGMGVR
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    SGTDVDAANLRETFTNLKYEVRNKNDLTREEILELMHSVSKEDHSKRSSFICVLLSHGEE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             F.M.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           00656; ICE_p20; 1.

PS01121; CASPASE_CYS; UNKNOWN_1.

PS01121; CASPASE_HIS; UNKNOWN_1.

PS01207; CASPASE_P10; 1.

PS50207; CASPASE_P20; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      (SEP-2001)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  277 AA; 31379 MW;
      Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Chordata;
Primates;
                    44.6%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            44.7%;
52.6%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   6
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      48,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  41;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               EMBL/GenBank/DDBJ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Last sequence update)
Last annotation updat
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Created)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Score 720.5; Pred. No. 7.1e
Score 719; DB 4;
Pred. No. 9.8e-58;
8; Mismatches 73
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Craniata; Vertebrata; Euteleostomi; Catarrhini; Hominidae; Homo.
                                                                                      1.
6162767B0D2DE021 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           1.
616C0F56141B012B CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    277
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         301
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    '.le-58;
les 74;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   DΒ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 databases
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                                         Length 277;
  Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Indels
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 277;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       15;
20;
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Gaps
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                                                                                                            Query Match
Best Local Sim
Matches 124;
                                                                                                                                                                                                                                                                                                             Denis F., Alam A., Cohen L., Harty Fortin J.-P., Sekaly R.-P.;
"Multiple Pathways of Apoptosis Committed (JUL-1996) to the EMBL/(EMBL; U63720; AAD09504.1; -.
HSSP: P42574; IPAU.
                                                                                                                                                                                                                                         MEROPS; C14.003; -...
MGD; MGI:107739; Casp3.
InterPro; IPR002238; ICE.
InterPro; IPR002138; ICE_p10.
InterPro; IPR001309; ICE_p20.
Pfam; PF00655; ICE_p10; 1.
Pfam; PF00656; ICE_p20; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                       Q9QWI4;
01-MAY-2000
01-MAY-2000
01-JUN-2002
                                                                                                                                                   Protease.
NON_TER
SEQUENCE
                                                                                                                                                                                  PROSITE;
PROSITE;
PROSITE;
PROSITE;
                                                                                                                                                                                                                                                                                                                                                                                                        Eukaryota;
Mammalia; |
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Q9QWI4
                                                                                                                                                                                                                       PRINTS; PR00376; ILIBCENZYME. SMART; SM00115; CASC; 1.
                                                                                                                                                                                                                                                                                                                                                                          SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                              NCBI_TaxID=10090
                                                                                                                                                                                                                                                                                                                                                                                                                          Mus musculus (Mouse).
                                                                                                                                                                                                                                                                                                                                                                                                                                             CPP32 apoptotic
                                                    142
             202
                                62
                                                                              229
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                                                                    TGMSARNGTDVDAANLRETFMGLKYQVRNKNDLTREDILELMDSVSKEDHSKRSSFVCVI
INDTDANPR-YKIPVEADFLFAYSTVPGYYSWRSPGRGSWFVQALCSILEEHGKELEIMQ
                           LSHGDEGVIYGTNGPVELKKLTSFFRGDYCRSLTGKPKLFIIQACRGTELDCGIETDSG-
                                         LSHGEENVIYGKDGVTPIKDLTAHFRGDRCKTLLEKPKLFFIQACRGTELDDAIQADSGP 201
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              KLEFMHILTRVNRKVATEFESFSFDATFHAKKQIPCIVSMLTKELYF
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ELEIMQILTRVNDRVARHFESQSDDPHFHEKKQIPCVVSMLTKELYF
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   NKNFHKSTGMTSRSGTDVDAANLRETFRNLKYEVRNKNDLTREEIVELMRDVSKEDHSKR
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              NKNFDKVTGMGVRNGTDKDAEALFKCFRSLGFDVIVYNDCSCAKMQDLLKKASEEDHTNA 134
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       EDSVDAKPDRSSEVPSLESKKKKNVTMRSI--KTTRDRVPTYQ--YNMNFEKLGKCIIIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ACFACILLSHGEENVIYGKDGVTPIKDLTAHFRGDRCKTLLEKPKLFFIQACRGTELDDA
                                                                                                            Similarity 56.24; Conservative
                                                                                                                                                                                PS01122; CASPASE_CYS;
PS01121; CASPASE_HIS;
PS50207; CASPASE_P10;
PS50208; CASPASE_P20;
                                                                                                                                                                                                                                                                                                                                                                                                      Eutheria;
                                                                                                                                                    220
                                                                                                                                                                                                                                                                                                                                                                                                                                                      (TrEMBLrel. 13, Created)
(TrEMBLrel. 13, Last sequence up)
(TrEMBLrel. 21, Last annotation
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              PRELIMINARY;
                                                                                                                                                   ΑA;
                                                                                                                                                                                                                                                                                                                                                                                                                                             protease
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25050
                                                                                                                                                                                                                                                                                                                                                                                                      Chordata;
Rodentia;
                                                                                                                      38.7%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          SKSIKNLEPKIIHGSESMDSGMSWDTGYKMDYPEMGLCIIIN
                                                                                                                                                                                                                                                                                                                                                                                                                                             (Fragment).
                                                                                                                                                   ₩;
                                                                                                             29;
                                                                                                           Score 623.5;
Pred. No. 4e-4
29; Mismatches
                                                                                                                                                                                                                                                                                                                                   osis Converging on EMBL/GenBank/DDBJ
                                                                                                                                                                                                                                                                                                                                                              Hartgers
                                                                                                                                                                                                                                                                                                                                                                                                    Craniata; Vertebrata;
Sciurognathi; Muridae
                                                                                                                                                   FE7F4857C4EBA544 CRC64;
                                                                                                                                                                                  ----
                                                                                                                     623.5;
No. 4e-
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             220
                                                                                                                     .5; DB 11;
4e-49;
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                                                                                                                                                                                                                                                                                                                                                               Braun
                                                                                                                                                                                                                                                                                                                                                                                                       Muridae;
                                                                                                             63;
                                                                                                                                                                                                                                                                                                                                   the CPP32 databases.
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                                                                                                           Indels
                                                                                                                             Length
                                                                                                                                                                                                                                                                                                                                                                Martinez
                                                                                                                                                                                                                                                                                                                                                                                                                Euteleostomi;
                                                                                                                                                                                                                                                                                                                                                                                                      Murinae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               275
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                                                                                                                               220;
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                                                                                                           Gaps
                             120
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Вb
                                                                                                                                                                                                  Matches
                                                                                                                                                                                                                      Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            093415;
                                                                                                                                                                                                                                       PROSITE; PS01122; CASPASE_CYS; 1.
PROSITE; PS50207; CASPASE_P10; 1.
PROSITE; PS50208; CASPASE_P20; 1.
SEQUENCE 304 AA; 34534 MW; 51CE31EBCAAE7383 CRC64;
                                                                                                                                                                                                                                                                                                                                                                         "Caspase-6 gene disruption reveals a requirement in apptictic chromatin condensation."; EMBO J. 21:1967-1977(2002). EMBL; AF082329; AAC32378.1; -. EMBL; AF469049; AAL82386.1; -.
                 243
                                                                                                                                                                                                                                                                                                     Pfam; PF00655; ICE_p10; 1.
Pfam; PF00656; ICE_p20; 1.
                                                                                                                                                                                                                                                                                                                      InterPro; IPR002398; ICE.
InterPro; IPR002138; ICE_p10.
InterPro; IPR001309; ICE_p20.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Biol. Reprod. 62:589-598(2000).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       cells."
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              "Caspase-3 and -6 expression and enzyme activity in
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    SEQUENCE FROM N.A.
MEDLINE=20149872; PubMed=10684799;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Archosauria; Aves; Neognathae; Galliformes; Phasianidae; Phasianinae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Gallus gallus (Chicken).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Caspase-6
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             01-NOV-1998 (TremBLrel. 01-JUN-2002 (TremBLrel.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         01-NOV-1998
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   01-NOV-1998
                                     181
                                                                             121
                                                                                                                                                                                                                                                                                                                                                        MEROPS; C14.005;
                                                                                                                                                                                                                                                                                                                                                                                                                            Kaufmann
                                                                                                                                                                                                                                                                                                                                                                                                                                    Ruchaud S., Korfali N.,
                                                                                                                                                                                                                                                                                                                                                                                                                                               PubMed=11953316
                                                                                                                                                                                                                                                                                                                                                                                                                                                           SEQUENCE FROM
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                SEQUENCE FROM
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  NCBI_TaxID=9031;
                                                         192
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Johnson A.L., Bridgham J.T.
                                                                                                132
                                                                                                                    64
                                                                                                                                                                               16
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          178
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                                                                                                                                        75
                                                                                                                                                                                                            Local Similarity
                                                                                                                                                            9
    QALCSILEEHGKELEIMQILTRVNDRVÄRHFESQSDDPHFHEKKQIPCVVSMLTKELYF
                                DDPVLVQDSVDSKDETTVNQTEVDAAGVYTLPAGADFIMCYSVAQGYFSHRETVNGSWYI 240
                                                                        SNADCFVCVFLSHGENDHVYAYDAQIKIETITNMFRGDKCQSLVGKPKIFIIQACRGDKH 180
                                                                                            TNAACFACILLSHGEENVIYGKDGVTPIKDLTAHFRGDRCKTLLEKPKLFFIQACRGTEL
                                                         DDAI -----
                                                                                                                HEHFFWHLRLPDRRGTLADRNNLKRSLTDLGFEVRIFDD---LKAEDVLKKVFEASRDDY 120
                                                                                                                                NKNFDKVTGMGVRNGTDKDAEALFKCFRSLGFDVIVYNDCSCAKMQDLLKK---ASEEDH
                                                                                                                                                        AAGRVQLDSKP----TPTTTADGNQNITEVDAFDKRRTFDPAEQYKMNHQRRGVALIFN
                                                                                                                                                                         SANEDSVDAKPDRSSFVPSLFSKKKKNVT-MRSIKTTRDRVPTYQYNMNFEKLGKCIIIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ILTRVNRKVATEFESFSLDSTFHAKKQFPCIVSMLTKELYF 218
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ILTRVNDRVARHFESQSDDPHFHEKKQIPCVVSMLTKELYF
                                                                                                                                                                                                   114;
                                                                                                                                                                                                                                                                                                                                                                 P42574;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ---TDEEMACQKIPVEADFLYAYSTAPGYYSWRNSKDGSWFIQSLCSMLKLYAHKLQFMH
                                                                                                                                                                                                                                                                                ; PR00376; ILIBCENZYME. SM00115; CASC; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                          S.H., Earnshaw
                                                                                                                                                                                                  Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 (TrEMBLrel.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     PRELIMINARY;
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                                                     -QADSGPINDT--DANPRYKIPVEADFLFAYSTVPGYYSWRSPGRGSWFV 242
                                                                                                                                                                                                            31.8%;
38.1%;
                                                                                                                                                                                                                                                                                                                                                                                                                           W.C.;
                                                                                                                                                                                                                                                                                                                                                                                                                                    Villa P., Kottke T.J.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             08,
21,
                                                                                                                                                                                                 51;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Last sequence update)
Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Created)
                                                                                                                                                                                                           Score 512.5;
Pred. No. 9.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      PRT;
                                                                                                                                                                                                 Mismatches
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                                                                                                                                                                                                                   DB 13;
                                                                                                                                                                                                113;
                                                                                                                                                                                                                                                                                                                                                                                                                                   Dingwall
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                                                                                                                                                                                              Gaps
             301
                                                                                                                                    131
                                                                                                                                                         63
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  RESULT 11
Q918S9
ID Q918S
AC Q918S
DT 01-OC
DT 01-OC
DT 01-MA
DE Caspa
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Q918S9;
01-OCT-2000 (
01-OCT-2000
01-MAR-2002
Caspase 6.
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RESULT
Q9IB66
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Best Local
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PROSITE; PS01122; CASPASE_CYS; 1

PROSITE; PS01121; CASPASE_HIS; 1

PROSITE; PS50207; CASPASE_P10; 1

PROSITE; PS50208; CASPASE_P20; 1

SEQUENCE 303 AA; 34132 MW; 4
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Q9IB66;
Q9IB66;
01-OCT-2000
Q918S9
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       InterPro; IPR001309; ICE_p20.
Pfam; PF00655; ICE_p10; 1.
Pfam; PF00656; ICE_p20; 1.
PRINTS; PR00376; IL1BERIZYME.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       family.";
J. Biol. Chem
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        EMBL; AB038169;
HSSP; P42574; 10
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 SEQUENCE FROM N.A. MEDLINE=20209426; Pubmed=10744739.
                                                                                 247
                                                                                                                                            187
                                                                                                                                                                            196
                                                                                                                                                                                                           127
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       InterPro; IPR002398; InterPro; IPR002138; InterPro; IPR001309;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          MEROPS; C14.005;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Nakajima K., Takahashi
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                NCBI_TaxID=8355;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Eukaryota; Metazoa; Chordata;
Amphibia; Batrachia; Anura; Me
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Xenopus laevis (African clawed frog).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                01-MAR-2002
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                01-OCT-2000
                                                                                                                                                                                                                                          137
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Kenopodinae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 KCASPASE-6.
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                                                                                                                                                                                                                                                                                                                                      16
                                                                                                                                                                                                                                                                                                                                                                     19
                                                                                                                                                                                                                                                                                                                                                                                                                 Local Similarity
                                                                           KAYAASLEFTEILTLVNRKVSQRSVEYCNDPKAIGKKQIPCFASMLTKKLF
                                                                                                                                       PKDEVDSVPLTNVTEVDAASLCTLPAGADFINCYSVAEGYYSHRETVNGSWYIQDLCAVV
                                                                                                                                                                   ---QADSGP---INDTDANPRYKIPVEADFLFAYSTVPGYYSWRSPGRGSWFVQALCSIL
                                                                                                                                                                                                    FICVFLSHGEDKHIYSYDSLIDIQELINPFKGDKCKSLVGKPKIFILQACRGEKHDEPVL
                                                                                                                                                                                                                                                                                                                                                             EDSVDAKPDRSSFVPSLFSKKKKNVTMRSIKTTR--DRVPTYQYNMNFEKLGKCIIINNK 76
                                                                                                        EEHGKELEIMQILTRVNDRVARHFESQSDDPHFHEKKQIPCVVSMLTKELY 300
                                                                                                                                                                                                                                   FACILLSHGEENVIYGKDGVTPIKDLTAHFRGDRCKTLLEKPKLFFIQACRGTELDDAI- 195
                                                                                                                                                                                                                                                                    DFYWQLRLGSRRGTNTDSMNLNRILTDLGFDVQNYYNLRTMDVLEKIQEASTTDHSNADC
                                                                                                                                                                                                                                                                                                  NFDKVTGMGVRNGTDKDAEALFKCFRSLGFDVIVYNDCSCAKMQDLLKKASEEDHTNAAC
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                                                                                                                                                                                                                                                                                                                                                                                                    108;
 PRELIMINARY;
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                                                                                                                                                                                                                                                                                                                                                                                                  Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                              31.6%;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   A., Yaoita Y and function
                                                                                                                                                                                                                                                                                                                                  -EQKANVTETDGWTSRTVELDPSAEYIMTHKRRGLALIFNHE
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20,
                                                                                                                                                                                                                                                                                                                                                                                                  59;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ); Craniata; Ver
Mesobatrachia;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Last sequence update)
Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Created)
                                                                                                                                                                                                                                                                                                                                                                                                                 Score 510;
Pred. No. 1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            PRT;
                                                                                                                                                                                                                                                                                                                                                                                                 red. No. 1.5e-38;
mismatches 106
                                                                                                                                                                                                                                                                                                                                                                                                                                                               4C54A0A607C69756 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ۹ Y.;
 302
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B
                                                                                                                                                                                                                                                                                                                                                                                                                                DB 13;
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                                                                                                                                                                                                                                                                                                                                                                                                 106;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Pipoidea;
                                                                                                                                                                                                                                                                                                                                                                                                                            Length
                                                                                                                                                                                                                                                                                                                                                                                               Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Euteleostomi;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Pipidae;
                                                                                                                                                                                                                                                                                                                                                                                                                              303;
                                                                           297
                                                                                                                                                                                                                                                                                                                                                                                                 18;
                                                                                                                                                                                                                                                                                                                                                                                            Gaps
                                                                                                                                                                     249
                                                                                                                                                                                                      186
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4;

(TrEMBLrel. (TrEMBLrel.

15, 15, 20,

Created)
Last sequence update)
Last annotation updat

update)

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RESULT 12
077623
ID 07762
AC 07762
AC 07762
DT 01-NO
DT 01-MA
DE Caspa
OS Ovis
OC Eukar
OC Mamma
OC Bovid
OX NCBI_
RN (1)
RP SEQUE
RA Rueda
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Query Match
Best Local S
Matches 108
                                   Ovis aries (Sheep).

Eukaryota; Metazoa; Chordata; Craniata; Vertebra: Mammalia; Eutheria; Cetartiodactyia; Ruminantia; Bovidae; Caprinae; Ovis.

RCBI_TaxID=9940;
                                                                                                             01-NOV-1998 (TrEMBLrel.
01-NOV-1998 (TrEMBLrel.
01-MAR-2002 (TrEMBLrel.
              SEQUENCE FROM N.A.
                                                                                                     Caspase-3
                                                                                                                                                                  077623
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               PROSITE;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        PROSITE; PROSITE;
                                                                                                                                                       077623;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Pfam; PF00655; ICE_p10; 1.
Pfam; PF00656; ICE_p20; 1.
PRINTS; PR00376; IL1BCENZYME.
SMART; SM00115; CASC; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Submitted (DEC-1999) to 1
EMBL; AF212219; AAF73848
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 "Cloning and sequencing mykiss, and analysis of
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Oncorhynchus mykiss (Rainbow trout) (Salmo gairdneri). Euteleost Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleost Actinopterygii, Neopterygii; Teleostei; Euteleostei; Protacanthopterygii; Salmoniformes; Salmonidae; Oncorhynchus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      MEROPS; C14.005;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        SEQUENCE FROM N.A.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   InterPro;
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                                                                                                                                                                                                                                                                                                                                 172
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                                                                                                                                                                                                                                                                                                                                                                                                           123
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                                                                                                                                                                                                                                                                                                                                                                                                                                    52
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                                                                                                                                                                                                                               TRKLYF
                                                                                                                                                                                                                                                       TKELYF 301
                                                                                                                                                                                                                                                                            INGSWYIQDLCGAMRKFGDSLEFTELLTLVNRKVSMRSVGNCNDKTAIGKKQVPCFASML
                                                                                                                                                                                                                                                                                                   GRGSWFVQALCSILEEHGKELEIMQILTRVNDRVARHFESQSDDPHFHEKKQIPCVVSML
                                                                                                                                                                                                                                                                                                                                                     IQACRGTELDDAIQ----ADSG-PIND--TDANPRYKIPVEADFLFAYSTVPGYYSWRSP
                                                                                                                                                                                                                                                                                                                                                                               ISQAAEANHADADCFVCVFLSHGENDHVYAYDDKIAIQDITALFKGDKCKSLVGKPKIFI
                                                                                                                                                                                                                                                                                                                                                                                                      LKKASEEDHTNAACFACILLSHGEENVIYGKDGVTPIKDLTAHFRGDRCKTLLEKPKLFF
                                                                                                                                                                                                                                                                                                                                                                                                                                NHKRRGLALIFNQEHFFWHLRMPPRNGTNADRSNLVKRFEDLNFEVQAFDNLKVEEVLDQ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        DDQGCIEEQGVEDSANEDSVDAKPDRSSFVPSLFSKKKKNVTMRSIKTTRDRVPTYQYNM
                                                                                                                                                                                                                                                                                                                               LQACRGDKHDDPVTPMDVVDSEVKTNEVVVDAGVVYTLPAGADFIMCYSVAEGYYSHRET
                                                                                                                                                                                                                                                                                                                                                                                                                                                        NFEKLGKCIIINNKNFDKVTGMGVRNGTDKDAEALFKCFRSLGFDVIVYNDCSCAKMQDL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  DTKGSLEKDNKTSQTTGPSENLTETDGYFCSSSFSMD--------
  B.R.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          K.J.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  P42574; 1PAU.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              PS01122; CASPASE_CYS;
PS01121; CASPASE_HIS;
PS50207; CASPASE_P10;
PS50208; CASPASE_P20;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 IPR002398;
IPR002138;
IPR001309;
                                                                                                  (Fragment).
 Hendry I.R.,
                                                                                                                                                                                                                               297
                                                                                                                                                                 PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Holland J.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     AΑ;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      34082
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              31.0%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ICE_p10
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ICE_p20
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          to the
                                                                                                               08,
20,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Bonilla
of caspa
its expr
Tilly J.L.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     MW;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   50;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 nilla S., Cunningham C., Secombes C.J.; caspase 6 in rainbow trout, Oncorhynchus s expression under conditions known to
                                                                                                             Created)
Last sequence update)
Last annotation updat
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          EMBL/GenBank/DDBJ databases
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Pred. No. 1.10); Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Score 500.5;
Pred. No. 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ; 1.
; 1.
; 1.
; 1.
5A6B5F2BA0CFA660 CRC64;
 Hamernik D.L.;
                                                                                                                                                              182
                                                                          Vertebrata; Euteleostomi;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               .1e-37
                                                                                                                                                              AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           DB 13;
                                                                                                              update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   125;
                                                              Pecora;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Length
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Euteleostomi;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  -PAEEYKM
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 23;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Gaps
                                                                                                                                                                                                                                                                             291
                                                                                                                                                                                                                                                                                                      295
                                                                                                                                                                                                                                                                                                                             231
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                                                                                                                                                                                                                                                                                                                                                                                171
                                                                                                                                                                                                                                                                                                                                                                                                       182
                                                                                                                                                                                                                                                                                                                                                                                                                                111
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RESULT
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Query Match
Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Query Match
Best Local :
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Matches
                             PROSITE;
SEQUENCE
                                                                                                                          InterPro;
InterPro;
                                                                                                                                                               Strausberg R.;
Submitted (JAN-2001)
EMBL; BC002022; AAH0
                                                                  PRINTS; PR00376; ILIBCENZYME SMART; SM00115; CASC; 1.
PROSITE; PS01122; CASPASE_CY:
                                                                                                                                                                                                                           Mus musculus (Mouse)
Eukaryota; Metazoa;
Mammalia; Eutheria;
                                                                                               Pfam; PF00655; ICE_p10; Pfam; PF00656; ICE_p20;
                                                                                                                                                         HSSP;
                                                                                                                                                                                                                                                                                    01-JUN-2001
01-JUN-2001
                                                                                                                                                                                                                                                                                                                   Q99M47
                                                 PROSITE;
                                                           PROSITE;
                                                                                                                                              MGD; MGI:1312921;
                                                                                                                                                                                               SEQUENCE FROM N.A.
                                                                                                                                                                                                                 NCBI_TaxID=10090,
                                                                                                                                                                                                                                                         CASP6
                                                                                                                                                                                                                                                                 Caspase
                                                                                                                                                                                                                                                                           01-MAR-2002
                                                                                                                                                                                                                                                                                                         Q99M47;
                                                                                                                    InterPro;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   PROSITE; PS01122; CASPASE_CYS; PROSITE; PS01121; CASPASE_HIS; PROSITE; PS50207; CASPASE_P10;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           PRINTS;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            PROSITE;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  SMART;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       InterPro; IPR002138;
InterPro; IPR001309;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          InterPro;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       EMBL; AF068837;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Submitted (MAY-1998)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Vivo."
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   NON_TER
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Pfam;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    MEROPS; C14.003;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              HSSP;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  "Accumulation of Caspase-3 mRNA and Induction of Caspase Activity the Ovine Corpus Luteum Following Prostaglandin-F2a Treatment In
                                                                                                                                                                                                                                                                                                                                                                  126
                                                                                                                                                                                                                                                                                                                                                                         180 LFFIQACRGTELDDAIQADSGPINDTDANPRYKIPVEADFLFAYSTVPGYYSWRSPGRGS
                                                                                                                                                                                                                                                                                                                                                                                                                          120
                                                                                                                                                                                                                                                                                                                                                                                                        66
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                                                                                                                                                                                                                                                                                                                                                             QDLLKKASEEDHTNAACFACILLSHGEENVIYGKDGVTPIKDLTAHFRGDRCKTLLEKPK
                                                                                                                                                                                                                                                                                                                                                                                                                                           YKMDYPEMGLCIIINNKNFHENTGMACRSGTDVDAANLRETFTSLKYEVRIKNDLTRKEM
                                                                                                                                                                                                                                                                                                                                                                                                       LELMSDVSKEDHSKRSSFICVLLSHGEEGIIFGTNGPVDLKKLASFFRGDCCRSLTGKPK
                                                                                                                                                         P42574; 1PAU
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  PF00655; ICE_p10; PF00656; ICE_p20;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             P42574; 1PAU
                                   ; PS01122; CASPASE_CYS;
; PS01121; CASPASE_HIS;
; PS50207; CASPASE_P10;
; PS50208; CASPASE_P20;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ; PR00376; IL1BC
SM00115; CASC;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   95;
                                                                                                                                                                                                                                                                  <u>о</u>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Similarity
                                                                                                                  IPR002398;
IPR002138;
IPR001309;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          PS50208; CASPASE_P20;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            IPR002398;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         182 AA;
                                                                                                                                                                                                                                                                                    (TrEMBLrel.
                                                                                                                                                                                                                                                                           (TrEMBLrel.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Conservative
                                                                                                                                                                                                                                                                                                                   PRELIMINARY;
                                                                                                                                                                  AAH02022
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     1998) to the AAC25713.1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           IL1BCENZYME
                                                                                                                                              Casp6
                                                                                                                                                                                                                          Chordata;
Rodentia;
                            31563 MW;
                                                                                                                 ICE_p10.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         20408 MW;
30.0%;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           30.6%;
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ICE_p20.
                                                                                                                                                                  the
2.1;
                                                                                                                                                                                                                                                                         17,
17,
20,
                                                                                                                                                                                                                                                                         Created)
Last sequence upo
Last annotation
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  30;
                                                                                                                                                                           EMBL/GenBank/DDBJ
Score
Pred.
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                        ; 1.
; 1.
; 1.
; 1.
; 1.
5965C5932A127B6C CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Pred. No. 2.6
0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Score 493.5;
Pred. No. 2.
                                                                                                                                                                                                                          Craniata; Vertebrata; Euteleostomi; Sciurognathi; Muridae; Murinae; Mus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        B5860C6996C21BE7 CRC64;
483.5; DB 11;
No. 3.6e-36;
                                                                                                                                                                                                                                                                                                                  276
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             .6e-37
                                                                                                                                                                                                                                                                                    update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    DB 6;
                                                                                                                                                                                                                                                                         update)
                                                                                                                                                                           databases
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     182;
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                                                                                                                                                                                Matches
                                                                                                                                                                                                Query Match
Best Local
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           035397;
035397;
01-JAN-1998
01-NOV-1998
01-MAR-2002
Caspase 6.
                                                                                                                                                                                                                                                   PROSITE; PS01122; CASPASE_CYS; PROSITE; PS01121; CASPASE_H10; PS0207; CASPASE_P10; PS50208; CASPASE_P20; CASPASE_P20;
                                                                                                                                                                                                                                                                                                                                                                                                                                Submitted (JUL-1998) to the EMBL/GenBank/DDBJ databases EMBL; AF025670; AAC25433.1; -. HSSP; P42574; IPAU.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                             STRAIN-SPRAGUE-DAWLEY; TISSUE-KIDNEY Kaushal G.P., Singh A.B., Shah S.V.; "Rat kidney Mch2.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Rattus norvegicus (Rat).
Eukaryota; Metazoa; Chordata;
Mammalia; Eutheria; Rodentia;
                                                                                                                                                                                                                                                                                                               PRINTS; PR00376; IL1BCENZYME SMART; SM00115; CASC; 1.
                                                                                                                                                                                                                                                                                                                                            Pfam; PF00655; ICE_p10; 1.
Pfam; PF00656; ICE_p20; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                        MEROPS; C14.005;
                                                                                                                                                                                                                                                                                                                                                                                        InterPro;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      NCBI_TaxID=10116;
136 GKPKIFIIQACRGSQHDVPLVPLDVVDHQTDKLDDNVTQVDAASVYTLPAGADFLMCYSV
                                   176
                                                                                            116
                                                                                                                                                                                                                                                                                                                                                                          InterPro;
                                                                                                                                                                                                                                                                                                                                                                                                       interPro;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             256 QVPCFASMLTKKLHF 270
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          287
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                           EKPKLFFIQACRGTELD-----DAIQADSGPIND----TDANPRYKIPVEADFLFAYST
                                                                                   CAKMODLLKKASEEDHTNAACFACILLSHGEENVIYGKDGVTPIKDLTAHFRGDRCKTLL 175
                                                                                                                  PAEQYKMDHKRRGTALIFNHERFFWHLALPERRGTNADRDNPTRRFSELGFEVKCFNDLR 75
                                                                                                                                            PTYQYNMNFEKLGKCIIINNKNFDKVTGMGVRNGTDKDAEALFKCFRSLGFDVIVYNDCS 115
                                                        AEELLLKIHEVSTSSHVDADCFLCVFLSHGEGNHIYAYDAKIEIQTLTGLFKGDKCQSLV
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             QIPCVVSMLTKELYF 301
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           GKPKIFIIQACRGSQHDVPVVPLDVVDHQTDKLDNVTQVDAASVYTLPAGADFLMCYSVA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   AEELLLKIHEVSTSSHIDADCFICVFLSHGEGNHVYAYDAKIEIQTLTGLFKGDKCQSLV 135
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                CAKMODILKKASEEDHTNAACFACILISHGEENVIYGKDGVTPIKDLTAHFRGDRCKTLL 175
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   EGYYSHRETVNGSWYIQDLCEMLARYGSSLEFTELLTLVNRKVSQRRVDFCKDPDAIGKK
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             PGYYSWRSPGRGSWFVQALCSILEEHGKELEIMQILTRVNDRVARHFESQSDDPHFHEKK 286
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        EKPKLFFIQACRGTELD------DAI--QADS-GPINDTDANPRYKIPVEADFLFAYSTV 226
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             PAEQYKMDHKRRGVALIFNHERFFWHLTLPERRGTNADRDNLTRRFSDLGFEVKCFNDLR 75
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          PTYQYNMNFEKLGKCIIINNKNFDKVTGMGVRNGTDKDAEALFKCFRSLGFDVIVYNDCS 115
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            100; Conservative
                                                                                                                                                                                              Similarity
                                                                                                                                                                                                                                                                                                                                                                      IPR002138; ICE_p10.
IPR001309; ICE_p20.
                                                                                                                                                                                                                                                                                                                                                                                                       IPR002398;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          3 (TrEMBLrel. 05, 3 (TrEMBLrel. 08, 20) (TrEMBLrel. 20,
                                                                                                                                                                                Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      PRELIMINARY;
                                                                                                                                                                                                                                         AA;
                                                                                                                                                                                                                                       31556 MW;
                                                                                                                                                                            29.8%; Score 481; DB 11; 38.7%; Pred. No. 6.2e-36; tive 43; Mismatches 104,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          43;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Created)
Last sequence update)
Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Craniata; Vertebrata; Euteleostomi; Sciurognathi; Muridae; Murinae; Rattus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    PRT;
                                                                                                                                                                                                                                      69D999E729B3BDE2 CRC64;
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Best Local S
Matches 98
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InterPro; IPR002138; ICE_p10.
InterPro; IPR002138; ICE_p20.
InterPro; IPR001309; ICE_p20.
Pfam; PF00655; ICE_p10; I.
Pfam; PF00656; ICE_p20; I.
PRINTS; PR00376; ILBCENZYME.
SMART; SM00115; CASC; I.
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SEQUENCE
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Q9BQE7;
Q1-JUN-2001 (TrEMBLrel. 17,
Q1-JUN-2001 (TrEMBLrel. 17,
Q1-JUN-2002 (TrEMBLrel. 21,
                                                                                                                                                                                                                                                                                                                                                                                                                         PROSITE; PS01122; CASPASE_CYS;
PROSITE; PS01121; CASPASE_HIS;
PROSITE: PS50207; CASPASE_P10;
PROSITE: PS50208; CASPASE_P20;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Submitted (NOV-2000) to the EMBL/GenBank/DDBJ databases EMBL; BC004460; AAH04460.1; -.
EMBL; BC000305; AAH00305.1; -.
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Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
 273
                                                                213
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             KQIPCVVSMLTKELYF
                                                                                                                                                                                        AEELLLKIHEVSTVSHADADCFVCVFLSHGEGNHIYAYDAKIEIQTLTGLFKGDKCHSLV
KQVPCFASMLTKKLHF
                                                           AEGYYSHRETVNGSWYIQDLCEMLGKYGSSLEFTELLTLVNRKVSQRRVDFCKDPSAIGK
                                                                                  VPGYYSWRSPGRGSWFVQALCSILEBHGKELEIMQILTRVNDRVARHFESQSDDPHFHEK
                                                                                                                        GKPKIFIIQACRGNQHDVPVIPLDVVDNQTEKLDTNITEVDAASVYTLPAGADFLMCYSV
                                                                                                                                                      EKPKLFFIQACRGTE-----LDDAIQADSGPINDTDANPRYKIPVEADFLFAYST 225
                                                                                                                                                                                                                       CAKMODLLKKASEEDHTNAACFACILLSHGEENVIYGKDGVTPIKDLTAHFRGDRCKTLL 175
                                                                                                                                                                                                                                                       PAEKYKMDHRRRGIALIFNHERFFWHLTLPERRGTCADRDNLTRRFSDLGFEVKCFNDLK 92
                                                                                                                                                                                                                                                                                       PTYQYNMNFEKLGKCIIINNKNFDKVTGMGVRNGTDKDAEALFKCFRSLGFDVIVYNDCS
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98; Conserv
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Last annotation update)
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Search completed: December 2, 2002, 12:58:10 Job time: 29.7328 secs

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Minimum
Maximum
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Maximum Match 100%
Listing first 45 summaries
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Match
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1613
          1: \SID52\gcgdata\geneseq\geneseqp-embl\AA1980.DAT:*
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6: \SID52\gcgdata\geneseq\geneseqp-embl\AA1985.DAT:*
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8: \SID52\gcgdata\geneseq\geneseqp-embl\AA1989.DAT:*
9: \SID52\gcgdata\geneseq\geneseqp-embl\AA1989.DAT:*
10: \SID52\gcgdata\geneseq\geneseqp-embl\AA1999.DAT:*
11: \SID52\gcgdata\geneseq\geneseqp-embl\AA1991.DAT:*
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1: /SIDS2/qcadata/
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Copyright (c) 1993 - 2002 Compugen
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/SIDS2/gcgdata/geneseq/geneseqp-embl/AA2002.DAT:*
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AAW15262
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ABJ01222
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                                                                                                                                                                                                                                                                         Description
                                                                                                                             Human
                                                                                                                                                                           Amino
                                                                                                                                                                                               Cysteine protease
Apototic protease
                                                                               Human
                                                     Human
                                                                                                      Human
                                                                                                                                                         Human
                                                                                                                                                                                                                                                                                                                                                                                                                      being printed,
o acid sequenc
caspase-7.
caspase-7 SE
caspase 7 pr
caspase 7 pr
caspase 7 pr
interleukin-
caspase 7 pr
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ന	AAE06523	22	480	7	447.5
огу	AAW54392	19	389	7.	4
Human caspase 6 re	AA021925	23	293	8	466
caspase-	AAE00603	22	293	8	466
Apoptotic cysteine	AAW06244	18	293	28.9	466
leukin 1 c	AAY85062	21	401	9.	468
in 1 co	AAY85061	21	278	9	468
Human caspase-6 SE	ABJ01221	23	293	9.	474
Amino acid sequenc	AAY21720	20	293	9	474
spase 6 p	AA021924	23	276	0	83
ophila me	ABB61468	22	323	ω	N
la melano	ABB58379	22	339	ω.	539
rtate	AAW89198	20	299	4	552
e caspase 3	AAU05395	22	277	ω.	703
spase-3	AAB59579	22	245	ω	706
meric cassett	AAE00610	22	261	ω	707
rleuk	AAW47089	19	277	4	709
human	AAW48937	19	277	4	711
man ap	AAW48945	19	277	4	711
e-3. Unide	AAB98654	22	241	4.	716.5
	ABJ01218	23	277	4	718
caspase-3	AAE00600	22	277	4.	718
caspase 3	AAU05394	22	277	4	718
acid sequ	AAY21717	20	277	4.	718
in CP	AAW16600	17	277	4	718
man	AAB26763	21	249	4	19
caspas	AAG78712	22	277	4	\sim
acid	AAW41688	19	277	4	721
n interleukin	AAR95831	17	277	4.	721
. Homc	AAW00677	17	277	4	721
in CPP32beta	AAW00372	17	277	4	721
caspase 7	ABB78587	23	253	œ	4.1
ine proteas	AAW15263	18	253	8	8
ase-7.	AAB98655	22	244	80.8	1304
	8	23	340	ω̈	1.5

ALIGNMENTS

RESULT 1 AAW15247

AAW15247 standard; Protein; 303 AA

21-JUL-1997 AAW15247;

(first entry)

Cysteine protease; CMH-1; CPP32/Mch2 homologue-1; apoptos programmed cell death; cancer; neurodegenerative disease; autoimmune disease; gene therapy; diagnosis. 09-MAY-1997 Key W09716552-A1 Active-site Protein Protein Cysteine protease CMH-1. Active-site Peptide Homo sapiens /note= 155 /label= Mat_protein
/note= "active CMH-1 polypeptide (Claim 3)"
29..303 /note= "Hisl44 is a catalytic residue" 186 /note= "Cys186 is a catalytic residue" Location/Qualifiers /label= Pro-peptide 'label= - Mat_protein
"active CMH-1 polypeptide (Claim apoptosis;

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AAW15262
ID AAW1
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AC AAW1
XX
DT 05-A
XX
AC APOT
XX
KW MCh33
KW neur
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Best Local S
Matches 301
Mch3-alpha; cysteine protease;
neurodegenerative disease; the;
                                    Apototic protease Mch3-alpha.
                                                               05-AUG-1997
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           16-NOV-1995;
03-NOV-1995;
06-NOV-1995;
                                                                                       AAW15262;
                                                                                                             AAW15262 standard;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               or inactivated forms of CMH-1 can be expressed in prokaryotic or eukaryotic host cells. The polypeptides are useful for screening potential apoptosis inhibitors and for raising antibodies used to assay CMH-1, to regulate cholesterol levels, inhibit CMH-1 activity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            A PIOENZYME (AAWI324/) is activated to CMH-1, or CPP32/Mch2 homologue-1, a human cysteine protease that is involved in apoptosis. Its amino acid sequence was deduced from a full-length isolated CDMN along (NECCO).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Claim
                                                                                                                                                                         301
                                                                                                                                                                                               301
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      A proenzyme (AAW15247) is activated
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   DNA encoding active, activatable or inactive cysteine - useful in gene therapy for promoting and inhibiting for diagnosing cells with potential for apoptosis
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Lippke JA,
                                                                                                                                                                                                                         241
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             01-NOV-1996;
                                                                                                                                                                                                                                                                                                                                             121
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             solated cDNA clone (AAT66970). Active, activatable (i.e. proenzyme)
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                                                                                                                                                                                                                                                                                                                                                                                             61
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                                                                                                                                                                                                                              FVQALCSILEEHGKELEIMQILTRVNDRVARHFESOSDDDHFHEKKQIPCVVSMLTKELY
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                                                                                                                                                                                                                  FVQALCSILEEHGKDLEIMQILTRVNDRVARHFESQSDDPHFHEKKQIPCVVSMLTKELY
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DB; AAT66970.
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                                                                                                                                                                         303
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  303 AA;
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                                                             (first
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      apoptosis, and to purify CMH-1 polypeptides.
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95US-0007211.
95US-0007251.
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                                                                                                           Protein;
                                                           entry)
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99.3%;
therapy; diagnosis.
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Pred. No. 1.4e
1; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                  1;
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l.4e-161;
           ischaemia;
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Best Local Similarity 99.0
Matches 301; Conservative
                                                                                                                                                                                                                                          Human Mch3-alpha (AAW15262) is an apoptotic protein and novel member of the interleukin-1-beta converting enzyme (ICE) family of cysteine proteases. Its amino acid sequence was deduced from a cDNA clone (AAT66992) obtd. from a Jurkat library. Mch3-beta (AAW15263) has also been identified that lacks the active site of Mch3-alpha. Mch3-alpha polypeptides can be produced in engineered host cells and used to treat human diseases associated with cell death, such as AIDS, ischaemic injury, neurodegenerative diseases, etc. They can also be used to regulate apoptosis and to screen for Mch3-alpha.
                                                                                                                                                                                                                  Sequence
                                                                                                                                                                                                                                                                                                                                                                                 New gene encoding Mch3, a cysteine protease that regulates - for treating human diseases associated with apoptosis, ar screening for antagonists and agonists of Mch3
                                                                                                                                                                                                                                       agonists
                                                                                                                                                                                                                                                                                                                                                            Claim 8; Fig 1; 52pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                Alnemri ES,
Tomaselli K;
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FFIQACRGTELDDAIQADSGPINDTDANPRYKIPVEADFLFAYSTVPGYYSWRSPGRGSW
                                            DLLKKASEEDHTNAACFACILLSHGEENVIYGKDGVTPIKDLTAHFRGDRCKTLLEKPKL
                                                                                                                                    MADDQGCIEEQGVEDSANEDSVDAKPDRSSFVPSLFSKKKKNVTMRSIKTTRDRVPTYQY
                                 DLLKKASEEDHTNAACFACILLSHGEENVIYGKDGVTPIKDLTAHFRGDRCKTLLEKPKL
                                                                                         NMNFEKLGKCIIINNKNFDKVTGMGVRNGTDKDAEALFKCFRSLGFDVIVYNDCSCAKMQ
                                                                                                                        1997-289289/26
                                                                             NMNFEKLGKCIIINNKNFDKVTGMGVRNGTDKDAEALFKCFRSLGFDVIVYNDCSCAKMQ
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                                                                                                                                                                                                                                       and antagonists.
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JEFFERSON THOMAS
                                                                                                                                                                                                                 AA;
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184..188
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199..3(
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Pred. No. 1.4e
1; Mismatches
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l.4e-161;
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                                                                                                                                                                                                                                                                                                                                                                                              es apoptosis
and
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RESULT 3
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                                                                   Query Match
Best Local
                                                      Matches
                                                                                                                                                                                                                Rev-caspases are cysteine proteases that specifically cleave proteins after Asp residues and is expressed as a zymogen, in which the small subunit is N-terminal to a large subunit. A gene delivery vehicle comprising a rev-caspase coding sequence is useful for the treatment of cancer, where the gene delivery vehicle is internalised by tumour cells. The gene delivery vehicle is internalised by tumour cells transfected with a rev-caspase expressing vector can be used in identification of inhibitors or enhancers of caspase-mediated apoptosis.
                                                                                                         Sequence
                                                                                                                                      gene
                                                                                                                                                enhancer of caspase processing activity. Caspase inhibitors are useful for treating neurodegenerative diseases as well as for inhibiting apoptosis in the heart following myocardial infarction. Sequences AAX81217 -AAX81226 represent human caspase genes encoding caspase 1-10
                                                                                                                                                                                                                                                                                                                                                           Disclosure; Fig 17A-B;
                                                                                                                                                                                                                                                                                                                                                                                       cancer
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               autoimmune disease;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Amino acid sequence of caspase-7
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                                                                                                                                                                                                      In vitro translated rev-caspase can be used to identify an inhibitor
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                           1
                                                                                                                                                                                                                                                                                                                                                                                    isolated nucleic acid molecule encoding a rev-caspase - used screening and identifying inhibitors or enhancers for treating ser or autoimmune disease
                                                                                                                                                                                                                                                                                                                              invention relates to nucleic acid molecules encoding rev-caspases
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               FVQALCSILEEHGKELEIMQILTRVNDRVARHFESQSDDPHFHEKKQIPCVVSMLTKELY 300
            MADDQGCIEEQGYEDSANEDSVDAKPDRSSFVPSLFSKKKKNYTMRSIKTTRDRVPTYQY 60
                                                                                                                                                                                                                                                                                                                                                                                                                                             1999-419353/35
DB; AAX81223.
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MADDQGCIEEQGVEDSANEDSVDAKPDRSSFVPSLFSKKKKNVTMRSIKTTRDRVPTYQY
                                                                                                                                    products (AAY21715-Y21724).
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                                                                 Similarity
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                                                    Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               JEFFERSON THOMAS
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                                                                99.6%;
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1.4e-161;
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RESULT 4
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                                                                        Novel fusion polypeptide comprising first and second caspase subunit separated by cleavage site not associated in nature with caspase subunit, useful for cloning gene encoding enzymes involved in
                                                                                                                                                                                                                                                                                                                                                                       Human; caspase-7; interleukin-1 converting enzyme; ICE-LAP3; CHM-1; Mr cysteine protease; apoptosis; caspase expression cassette; metastasis; tumour; cathepsin B; urokinase; proliferation; gene therapy.
                                              Claim
                                                                                                                                              Cordell B,
                                                                                                                                                                                   20-OCT-1999; 99US-0160559
14-AUG-2000; 2000US-0225564
                                                                                                                                                                                                                                                                                    Cleavage-site
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                                                                 proteolytic cleavage
                                                                                                                  N-PSDB;
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                                                                                                                                                                 (SCIO-) SCIOS INC
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DB; AAD03914.
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                                                                                                                                              Li Y;
                                             14; 116pp;
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                                                                                                                                                                                                                                                                                    /label= Proteolytic_cleavage_site 206..207
                                                                                                                                                                                                                                                                                                        /label= Proteolytic_cleavage_site
198..199
                                                                                                                                                                                                                                                                                                                         Location/Qualifiers
23..24
                                                                                                                                                                                                                                                                          /label= Proteolytic_cleavage_site
                                             English
                                                                                                                                                                                                                                                                                                                                                                                             CHM-1; Mhc3;
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The present amino acid sequence is human Caspase-7 also known as interleukin-1 converting enzyme (ICE) LAP3, CHM-1 and Mhc3. Caspases a family of cysteine proteases, that participate in the initiation and

of apoptosis.

Caspases

exist as pro-enzymes,

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RESULT 5
ABJ01222
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6a-JAN-1999;
                                                                                                                                                                                                  Human caspase-7
                                                                                                                                                                                                                                                                           ABJ01222 standard;
                                                                                                              US6376226-B1
                                                                                                                                     Homo sapiens
                                                                                                                                                               cancer;
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 (UYJE-) UNIV
                                                            26-APR-2000;
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JEFFERSON THOMAS
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                                                           2000US-0561756
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           a large and small subunit, occurring after specific residues within the pro-enzyme sequence.
                        98US-070897P.
99US-0227721.
                                                                                                                                                                        rev-caspase;
                                                                                                                                                                                                 SEQ
                                                                                                                                                            disease;
                                                                                                                                                                                                                                                                            Protein; 303
                                                                                                                                                                                                 ID NO:
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99.3%;
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                                                                                                                                                           cytostatic;
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Pred. No. 1.4e
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                                                                                                                                                                        gene therapy; protease; apoptosis;
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L.4e-161;
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                                                                                                                    Caspase 7; antisense modulation; antiinflammatory; cytostatic; antisense therapy; caspase 7 inhibitor; inflammatory condition hyperproliferative disorder; cancer; bone metabolism; infectio cholesterol disorder; inflammation; tumour.
                                                21-MAR-2002
                                                                       WO200222640-A1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                The present invention provides the protein and coding sequences of human rev-caspase-3, uncleavable rev-caspase-3 and rev-caspase-6. The sequences can be used in the gene therapy of cancer and autoimmune diseases. The present sequence is a protein described in the exemplification of the
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     New rev-caspases engineered to contain the small subunit fused in N-terminal to the large subunit, which is in reverse order to the type caspases, are useful to treat cancer and autoimmune diseases {\sf table}
                      10-SEP-2001; 2001WO-US28232
                                                                                              Homo sapiens
                                                                                                                                                                                Human caspase 7 protein sequence
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Pred. No. 1.4e-161;
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Matches 301
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antisense therapy;
hyperproliferative
             Caspase 7; antisense modulation; antiinflammatory; cytostatic; antisense therapy; caspase 7 inhibitor; inflammatory condition
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                                                                                       (first
                                                       7 protein sequence SEQ
 caspase 7 disorder;
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99.3%;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          1;
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treating diseases associated
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                                                                                                                                                                                                                                                                                                                                                                                                                      sequence represents a human caspase 7 example from the present invention.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Novel antisense compounds targeted to nucleic acids encoding caspase for modulating gene expression and treating diseases associated with expression of caspase 7 in humans \cdot
                                                                                                                                                                                                                                                                                                                                                                                             Sequence
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Pred. No. 1.4e-161;
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                                                                                                                                                                                                                                                                                                                    specifically hybridises with and inhibits the expression of caspase 7 (I) has antiinflammatory and cytostatic activities, and can be used in antisense therapy and as an inhibitor of caspase 7 expression. (I) is useful for inhibiting the expression of caspase 7 in human cells or tissues, and for treating a human having a disease or condition, hyperproliferative disorder (cancer), or bone metabolism or cholesterol disorder. (I) is useful for diagnostics, therapeutics, prophylaxis and as research reagent and kits. (I) is useful prophylactically to prevent or delay infection, inflammation or tumour formation. The present sequence represents a human caspase 7 protein, which is used in an
                                                                                                                                                                                                                                                                                     Sequence
                                                                                                                                                                                                                                                                                                                 example
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Novel antisense compounds targeted for modulating gene expression and expression of caspase 7 in humans
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Example 15;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Caspase 7; antisense modulation; antiinflammatory; cytostatic; antisense therapy; caspase 7 inhibitor; inflammatory condition; hyperproliferative disorder; cancer; bone metabolism; infection; cholestarol disorder; information; cancer; bone metabolism; infection;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                The present invention describes a compound (I) 8-50 nucleob-
length targeted to a nucleic acid molecule encoding caspase
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                N-PSDB;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      (ISIS-)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         cholesterol disorder;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Caspase 7;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Human caspase
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                                                                                                                                            61
                                                                                                                                                                                                                   Local 301;
                                                                                                                  94
                                                                                                                                                                        34
                                                                                                                                                                                  1 MADDOGCIEEOGVEDSANEDSVDAKPDRSSFVPSLFSKKKKNVTMRSIKTTRDRVPTYQY 60
                                                                                                          NMNFEKLGKCIIINNKNFDKVTGMGVRNGTDKDAEALFKCFRSLGFDVIVYNDCSCAKMQ 120
              FFIQACRGTELDDAIQADSGPINDTDANPRYKIPVEADFLFAYSTVPGYYSWRSPGRGSW 240
                                                                   DLLKKASEEDHTNAACFACILLSHGEENVIYGKDGVTPIKDLTAHFRGDRCKTLLEKPKL
                                                                                                                                                                   MADDQGCIEEQGVEDSANEDSVDAKPDRSSFVPSLFSKKKKNVTMRSIKTTRDRVPTYQY 93
FFIQACRGTELDDGIQADSGPINDTDANPRYKIPVEADFLFAYSTVPGYYSWRSPGRGSW
                                                    DLLKKASEEDHTNAACFACILLSHGEENVIYGKDGVTPIKDLTAHFRGDRCKTLLEKPKL
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                                                                                                                                                                                                                                            Similarity
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                                                                                                                                                                                                                                                                                     336 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Page 103-105; 138pp;
                                                                                                                                                                                                                               Conservative
                                                                                                                                                                                                                                                                                                              the present invention.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           7 protein sequence
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                                                                                                                                                                                                                                         99.6%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        inflammation;
                                                                                                                                                                                                                         Score 1606; DI
Pred. No. 1.6e
1; Mismatches
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               to nucleic acids encoding
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                                                                                                                                                                                                                                         1.6e-161;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                             (I) 8-50 nucleobases in encoding caspase 7, which
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                                                                                                                                                                         Query Match
Best Local S
Matches 256
                                                                                                                                                                                                                                                    antitumor or antiviral agent and to control embryonic developm and tissue homeostasis. The protein can also be used to treat immunosuppression disorders, such as AIDS, by targeting virus infected cells for cell death. The DNA may find use in gene
                                                                                                                                                                                                                                                                                                                                          Human ICE-LAP-3 and -4 DNA and protein - useful in the diagnosis and treatment of Alzheimer's disease, Parkinson's disease, rheumatoid arthritis, septic shock and head injury
                                                                                                                                                                                                                    Sequence
                                                                                                                                                                                                                                                                                                 This ICE-LAP-3 protein may be used therapeutically,
                                                                                                                                                                                                                                                                                                                     Claim 1; Page 91-92; 67pp; English.
                                                                                                                                                                                                                                           therapy applications.
                                                                                                                                                                                                                                                                                                                                                                                          WPI; 1996-239509/24.
N-PSDB; AAT15276.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                        01-NOV-1994;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         W09613603-A1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ICE-LAP-3; interleukin-I-converting
enzyme; Alzheimer's disease; Parkins
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Human interleukin-I-converting enzyme-like apoptosis
185 ACRGTELDDAIQADSGPINDTDANPRYKIPVEADFLFAYSTVPGYYSWRSPGRGSWFVQA
                                                                                                                                                                                                                                                                                                                                                                                                                                                (HUMA-) HUMAN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      head injury; rheumatoid arthritis.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         28-OCT-1996
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                                                           125
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                                                                                                                                      QGCIEEQGVEDSANEDSVDAKPDRSSFVPSLFSKKKKNVTMRSIKTTRDRVPTYQYNMNF 64
                                              KASEEDHTNAACFACILLSHGEENVIYGKDGVTPIKDLTAHFRGDRCKTLLEKPKLFFIQ
                                                                              EKLGKCIIINNKNFDKVTGMGVRNGTDKDAEALFKCFRSLGFDVIVYNDCSCAKMQDLLK
                                                                                         EKLGKCIIINNKNFDKVTGMGVRNGTDKDAEALFKCFRSLGFDVIVYNDCSCAKMQDLLK
                                                                                                                          QGCIEEQGVEDSANEDSVDAKPDRSSFVPSLFSKKKKNVTMRSIKTTRDRVPTYQYNMNF 139
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             FSQ
                                 KASEEDHTNAACFACILLSHGEENVIYGKDGVTPIKDLTAHFRGDRCKTLLEKPKLFFIQ
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99.2%;
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                                                                                                                                                                      Score 1366; D
Pred. No. 4.7e
1; Mismatches
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           enzyme-like
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1.7e-136;
nes 1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   disease;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            apoptosis
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RESULT 10
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                                                                                                                                                                                                                              The present invention describes a compound (I) 8-50 nucleobases in clearly length targeted to a nucleic acid molecule encoding caspase 7, which expectifically hybridises with and inhibits the expression of caspase 7. (I) has antiinflammatory and cytostatic activities, and can be used in a nitisense therapy and as an inhibitor of caspase 7 expression. (I) is useful for inhibiting the expression of caspase 7 in human cells or tissues, and for treating a human having a disease or condition the expression of caspase 7 in condition associated with caspase 7 including inflammatory condition, hyperproliferative disorder (cancer), or bone metabolism or cholesterol disorder. (I) is useful for diagnostics, therapeutics, prophylaxis and as research reagent and kits. (I) is useful prophylactically to prevent or delay infection, inflammation or tumour formation. The present sequence represents a mouse caspase 7 protein, which is used in an certain continuous formation or tumour formation.
                                                                                                                                                 Query Match
Best Local
                                                                                                                                  Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Novel antisense compounds targeted to nucleic acids encoding caspase for modulating gene expression and treating diseases associated with expression of caspase 7 in humans \cdot
                                                                                                                                                                                                 Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Example 16;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     WPI; 2002-401902/43
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      (-SISI)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      cholesterol disorder; inflammation; tumour.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Mouse caspase 7 protein sequence SEQ ID NO:97
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                                  19
                                                                                                                                                   Local Similarity
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                 NMNFEKLGKCIIINNKNFDKVTGMGVRNGTDKDAEALFKCFRSLGFDVIVYNDCSCAKMQ 120
{\tt RMDFQKMGKCIIINNKNFDKATGMDVRNGTDKDAGALFKCFQNLGFEVTVHNDCSCAKMQ}
                                                               MTDDQDCAAELEKVDSSSEDGVDAKPDRSSIISSILLKKKRNASAGPVRTGRDRVPTYLY
                                                                                               MADDQGCIEEQGVEDSANEDSVDAKPDRSSFVPSLFSKKKKNVTMRSIKTTRDRVPTYQY
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                                                                                                                                                                                                   303
                                                                                                                                  Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Page 121-123; 138pp;
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                                                                                                                                                 83.4%;
                                                                                                                                  27;
                                                                                                                                               Score 1346; DB 23;
Pred. No. 5.2e-134;
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                                                                                                                                  Mismatches
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                                The present invention describes a compound (I) 8-50 nucleobases in length targeted to a nucleic acid molecule encoding caspase 7, which specifically hybridises with and inhibits the expression of caspase 7. (I) has antiinflammatory and cytostatic activities, and can be used in antisense therapy and as an inhibitor of caspase 7 expression. (I) is useful for inhibiting the expression of caspase 7 in human cells or tissues, and for treating a human having a disease or condition associated with caspase 7 including inflammatory condition, hyperproliferative disorder (cancer), or bone metabolism or cholesterol disorder. (I) is useful for diagnostics, therapeutics, prophylaxis and as research reagent and kits. (I) is useful prophylactically to prevent cellary infection, inflammation or tumour formation. The present example from the present invention.
                         example
                                                                                                                                                                                                                                                            Novel antisense compounds targeted for modulating gene expression and expression of caspase 7 in humans
                                                                                                                                                                                                                                                                                       Novel
                                                                                                                                                                                                                                                                                                                   N-PSDB;
                                                                                                                                                                                                                                                                                                                                                           Zhang H,
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 antisense therapy; caspase 7 inhibitor; inflammatory hyperproliferative disorder; cancer; bone metabolism;
                                                                                                                                                                                                                                  Example 13; Page 97-99; 138pp; English
                                                                                                                                                                                                                                                                                                                                                                                                                 11-SEP-2000; 2000US-0659860
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       cholesterol disorder; inflammation; tumour.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Mouse caspase 7 protein sequence
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DB; ABN80832.
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                                                                                                                                                                                                                                                                                                                                                                                      ISIS PHARM INC
                        from the present invention.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               7; antisense modulation; antiinflammatory; cytostatic;
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                                                                                                                                                                                                                                                                                                                                                           Watt AT;
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                                                                                                                                                                                                                                                              to nucleic acids a treating diseases
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                                                                                                                                                                                                                                                                           acids encoding caspase iseases associated with
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  condition;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     infection
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Sequence

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Best Local :
        The present invention relates to a molecule or molecular complex (I) comprising a binding pocket defined by the structure coordinates of caspase-7 amino acids 234, 235, 237, 276, 278, 281, and 284 or a homolo of (I) with a binding pocket having a root mean square deviation from t amino acid backbone atoms of not more than 1.5 Angstrom, where (I) has $4$ binding region that is more hydrophilic than that of caspase-3. The present sequence is caspase-7, which was used in a sequence homology alignment.
                                                                                                                            Molecule or molecular complex used for drug discovery, comprises a binding pocket of caspase-7 or a homolog having an S4 binding region more hydrophilic than that of caspase-3 -
                                                                                                                                                                                                                                                                                                                                                            Caspase-1; caspase-3.
                                                                                                          Example 4; Fig 3;
                                                                                                                                                                            WPI; 2001-329229/34.
                                                                                                                                                                                                                                             16-NOV-1999;
                                                                                                                                                                                                                                                                                         25-MAY-2001.
                                                                                                                                                                                                                                                                                                                                       Unidentified
                                                                                                                                                                                                                                                                                                                                                                                                                                                           AAB98655 standard; protein; 244 AA.
                                                                                                                                                                                                                                                                   16-NOV-2000;
                                                                                                                                                                                                                                                                                                                                                                                                                   16-AUG-2001
                                                                                                                                                                                                                                                                                                                                                                                                                                         AAB98655;
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247; Conserv
                                                                                                                                                                                                                      VERTEX
                                                                                                                                                                                                                                                                                                                                                                       Protein
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                                                                                                                                                                                                                                                                   2000WO-US31602
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                                                                                                                                                                                                                       PHARM INC
                                                                                                                                                                                                                                            99US-0165797
                                                                                                         161pp; English.
                                                                                                                                                                                                                                                                                                                                                                      co-ordinate
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Pred. No. 6.2e-134;
27; Mismatches 29;
                                                                                                                                                                                                                                                                                                                                                                     data; caspase-7; S4
                                                                                                                                                                                                                                                                                                                                                                    binding
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                                               from the
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RESULT 13
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Best Local Similarity
Matches 242; Conser
                      Claim
                                     New gene encoding Mch3, a cyst-
for treating human diseases
screening for antagonists and
                                                                     WPI; 1997-289289/26.
N-PSDB; AAT66993.
                                                                                              Alnemri ES,
Tomaselli K;
                                                                                                                                                                                                                                                                             Mch3-beta; cysteine protease; apoptosis; AIDS; neurodegenerative disease; therapy; diagnosis.
                                                                                                                      (UYJE-) UNIV
                                                                                                                                             13-NOV-1995;
                                                                                                                                                              12-NOV-1996;
                                                                                                                                                                              22-MAY-1997.
                                                                                                                                                                                              WO9718313-A1
                                                                                                                                                                                                                       Cleavage-site
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                                                                                                                                                                                                                                                                                                      Cysteine protease Mch3-beta
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                                                                                                                                                                                                                                                                                                                                                       standard;
                                                                                                                                                                                                                                                                                                                                                                                                              303
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                                                                                                     Armstrong
                                                                                                                      JEFFERSON THOMAS
                                                                                                                              PHARM INC
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                                                                                                                                                              96WO-US18118
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                                                                                                                                                                                                                                      Location/Qualifiers 24..28
                                                                                                                                                                                                                       /label= P20
54..58
                                                                                                                                                                                                              /label=
                                                                                                                                                                                                                                                                                                                                                       Protein;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    80.8%;
99.2%;
                      English
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                                     a cysteine protease that regulates apoptosis seases associated with apoptosis, and ts and agonists of Mch3
                                                                                                                                                                                                              P17
                                                                                                      Fernandes-Alnemri
                                                                                                                                                                                                                                                                                                                                                       253
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Score 1304; DB 22;
Pred. No. 1.1e-129;
1; Mismatches 1;
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Human Mch3-beta

n Mch3-beta (AAW15263) is a novel member of converting enzyme (ICE) family of cysteine

the interleukin-1-proteases. Its

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RESULT 14
ABB78587
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The present invention describes a compound (I) 8-50 nucleobases in length targeted to a nucleic acid molecule encoding caspase 7, which specifically hybridises with and inhibits the expression of caspase (I) has antiinflammatory and cytostatic activities, and can be used:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Caspase 7; antisense modulation; antiinflammatory; cytostatic; antisense therapy; caspase 7 inhibitor; inflammatory condition; hyperproliferative disorder; cancer; bone metabolism; infection
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                not include the QACRG active site pentapeptide sequence of Mch3-alpha. Mch3-beta polypeptides can be produced in engineered host cells. They can be used as dominant/negative inhibitors of apoptotic Mch3-alpha to treat or reduce the severity of diseases characterised by increased programmed cell death, such as AIDS, ischaemic injury, neurodegenerative diseases, etc., and can also
                                                                                                                                                                                                                                                                                                                                                                                                      WO200222640-A1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                    cholesterol disorder;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Human caspase 7 protein sequence SEQ
                                                                                                                                                                                                                                                                                                   11-SEP-2000; 2000US-0659860
                                                                                                                                                                                                                                                                                                                                 10-SEP-2001; 2001WO-US28232.
                                                                                                                                                                                                                                                                                                                                                                                                                                   Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     15-JUL-2002
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   from a Jurkat library. Mch3-beta mRNA arises from 2 simultaneous alternative splicing events that result in a shift in the reading frame after amino acid 148 of Mch3-alpha (AAW15262). Mch3-beta do
                                                                                                                  expression
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ABB78587 standard; Protein;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Sequence
                                                                                   Example 15;
                                                                                                                              Novel antisense compounds targeted to nucleic acids encoding caspase 7, for modulating gene expression and treating diseases associated with
                                                                                                                                                                                                                                                                  (ISIS-) ISIS PHARM
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    amino acid sequence was deduced from a cDNA clone (AAT66993) obtd. from a Jurkat library. Mch3-beta mRNA arises from 2 simultaneous
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      121
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      61
                                                                                                                 modulating gene expression and ression of caspase 7 in humans
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       NMNFEKLGKCIIINNKNFDKVTGMGVRNGTDKDAEALFKCFRSLGFDVIVYNDCSCAKMQ 120
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     DLLKKASEEDHTNAACFACILLSHGEENV 149
                                                                                                                                                                                   2002-401902/43.
DB; ABN80841.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    NMNFEKLGKCIIINNKNFDKVTGMGVRNGTDKDAEALFKCFRSLGFDVIVYNDCSCAKMQ 120
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                                                                                                                                                                                                                                   Watt AT;
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                                                                                Page 105-107; 138pp; English.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  for Mch3 agonists and antagonists.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  48.6%;
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Pred. No. 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ID NO:19
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RESULT 15
AAW00372
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Matches
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        useful for inhibiting the expression of caspase 7 in human cells or tissues, and for treating a human having a disease or condition associated with caspase 7 including inflammatory condition, hyperproliferative disorder (cancer), or bone metabolism or cholesterol disorder. (1) is useful for diagnostics, therapeutics, prophylaxis and as research reagent and kits. (1) is useful prophylactically to prevent or delay infection, inflammation or tumour formation. The present sequence represents a human caspase 7 protein, which is used in an
                                                                                                                                                                                                                                                                                                                                        pro-inflammatory; pro-apoptotic; apoptosis; inflammation; anti-
antisense DNA; treatment; immunne; proliferation; degeneration;
disease; AIDS; acquired immunodeficiency syndrome; autoimmune;
pathogenic infection; cardiovascular; neurological; injury;
alopecia; ageing; cancer; type I diabetes; Parkinson's;
                                                                                                                                                                                                                                                                                                                                                                                                                CPP23beta; isqform; inactive; CPP32; proenzyme: cysteine; protea proteolytic product; polyDP-ribose) polymerase; PARP; apopain; cleavage enzyme; human; monocytic leukaemia; cell line; THP-1; identification; modulator; recombinant production; gene therapy;
                                        Protein
                                                                                Region
                                                                                                                          Region
                                                                                                                                         Cleavage-site
                                                                                                                                                                                                                              Cleavage-site
                                                                                                                                                                                                                                                         Domain
                                                                                                                                                                                                                                                                        Key
                                                                                                                                                                                                                                                                                                    Homo
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                                                                                                                                                                       Protein
                                                                                                                                                                                                               Region
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    MADDQGCIEEQGVEDSANEDSVDAKPDRSSFVPSLFSKKKKNVTMRSIKTTRDRVPTYQY
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148; Conser
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175..176
176..193
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29..46
                                        176..277
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                                                                                                                                                                                                                                                                        Location/Qualifiers
                                                                   /note-
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99.3%;
                         "12 kDa subunit p12"
                                                                                                             "amino-terminal sequence
                                                                                                                                                                                                  "amino-terminal sequence determined
                                                                                                                                                                                                                                           "amino-terminal pro-domain'
                                                    "conserved pentapept
catalytic cysteine"
                                                                                              purified
                                                                                                                                                                                 purified
                                                                                                                                                     kDa subunit p17"
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Pred. No. 1.
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C apopain. The PARP cleavage enzyme was purified from the human c monocytic leukaemia cell line, THP-1, using standard ion exchange chromatography techniques and SDS PAGE. Apopain can be used to c identify apopain activity modulators, while apopain encoding DNA C may be used for apopain production or in gene therapy (i.e. in vivo c rex vivo gene transplantation) for enhancing the pro-inflammatory cor pro-apoptotic effects of apopain. Anti-apopain antibodies and c of apopain activity is beneficial in the treatment of immune.
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Best Local Similarity
Matches 144; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                              Sequence
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Apopain, a new human apoptosis related enzyme - responsible for the proteolytic breakdown of poly(ADP- ribose) polymerase (PARP) which occurs at the onset of apoptosis
                                                                                                                                     and Alzheimer's disease
                                                                                                                                                                                                                                                                                                                                                                                                                                                                            proliferative and degenerative diseases, e.g. AIDS, autoimmune disease, pathogenic infections, cardiovascular and neurological injury, alopecia, ageing, cancer, type I diabetes and Parkinson's
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               WPI; 1996-485775/48
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(MERI ) MERCK FROSST CANADA INC.
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                                259 MQILTRVNDRVARHFESQSDDPHFHEKKQIPCVVSMLTKELYF 301
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                                                                                                                                                                                                                               79 DKVTGMGVRNGTDKDAEALFKCFRSLGFDVIVYNDCSCAKMQDLLKKASEEDHTNAACFA 138
                                                                                                                                                                                                                                                                                                                 19 EDSVDAKPDRSSFVPSLFSKKKKNVTMRSIKTTRDRVPTVQYNMNFEKLGKCIIINNKNF 78
                                                                                                                                                                                                                                                                                       S
                                                                                    SGPINDTDANPRYKIPVEADFLFAYSTVPGYYSWRSPGRGSWFVQALCSILEEHGKELEI 258
MHILTRVNRKVATEFESFSFDATFHAKKQIPCIVSMLTKELYF
                                                               SGVDDDMAC---HKIPVEADFLYAYSTAPGYYSWRNSKDGSWFIQSLCAMLKQYADKLEF 232
                                                                                                                                                                                                                                                                                  ENSYDSKSIK-NLEPKIIHGSESMDSGISLDNS:-----YKMDYPEMGLCIIINNKNF 55
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50.9%; Pred. No. 9.1e-68;
tive 50; Mismatches 77;
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Search completed: December 2,

2002, 12:56:03

time: 34.9569 secs

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Result
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Maximum DB seq
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Copyright (c) 1993 - 2002 Compuç
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       /cgn2_6/ptodata/1/pubpaa/US08_FUBCOMB.pep:*
/cgn2_6/ptodata/1/pubpaa/US09_NEW_PUB.pep:*
/cgn2_6/ptodata/1/pubpaa/US09_NEW_PUB.pep:*
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10 US-09-895-263-2
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10 US-09-954-697-12
10 US-09-954-697-3
11 US-09-954-697-3
12 US-09-954-697-3
13 US-09-410-194-21
14 US-09-962-915-1
15 US-09-962-915-1
16 US-09-962-915-1
17 US-09-954-697-27
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              Sequence 2, Appli
Sequence 24, Appli
Sequence 4, Appli
Sequence 12, Appli
Sequence 21, Appli
Sequence 21, Appli
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Sequence 2, Appli
Sequence 20, Appli
Sequence 21, Appli
Sequence 21, Appli
Sequence 27, Appli
Sequence 29, Appli
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   Sequence
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45	44	43	42	41	40	39	38	37	36	ω 5	34	ω	32	31	30	29	28	27	26	25	24	23	22	21	20
209	210	210	221.5	224.5	241	251.5	251.5	252	252	255	258	258	263	264	264	300	308	317	321.5	332.5	342	342	347.5		357.5
13.0						15.6						16.0	16.3	16.4	16.4	18.6	•	19.7	•	20.6	•	•	21.5	•	22.2
214	418	47	410	410	51	260	257	242	229	242	242	242	300	81	52	163	451	435	167	182	503	354	416	416	479
10	10	10	10	10	10	10	10	10	10	10	10	10	10	10	10	10	10	10	10	10	10	10	10	9	10
US-09-989-903-9	US-09-954-697-18	US-09-989-903-36	US-09-917-265-15	US-09-917-265-24	US-09-989-903-41	US-09-989-903-2	US-09-764-803A-2	US-09-989-903-5	US-09-764-803A-4	US-09-845-028-2	US-09-845-028-9	US-09-764-803A-24	US-09-954-697-36	US-09-989-903-35	US-09-989-903-40	US-09-864-761-47950	US-09-888-243-28	US-09-954-697-9	US-09-864-761-48728	US-09-809-905-2	US-09-888-243-2	US-09-888-243-20	US-09-954-697-30	us-10-068-569-1	US-09-888-243-6
9, 4	18,		-		41,		2	Sequence 5, Appli	4	2,	Sequence 9, Appli	24,	36,	35,		479	28	Sequence 9, Appli	Sequence 48728, A	2,	2	20,	e 30	<u>, </u>	Sequence 6, Appli

ALIGNMENTS

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RESULT 1
US-09-895-263-2
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Patent No. US20020076793A1
GENERAL INFORMATION:
APPLICANT: He, Wei-Wu et al.
APPLICANT: He, Wei-Wu et al.
Like Apoptosis Protease 3 and 4
                                                                              INFORMATION FOR SEQ ID NO: 2:
SEQUENCE CHARACTERISTICS:
LENGTH: 303 amino acids
                                                                                                                                                                                                                                                                                             PRIOR APPLICATION DATA:
APPLICATION NUMBER: <Unknown>
FILING DATE: <Unknown>
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                     COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOETWARE: PATENTIAN Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/895,263
FILING DATE: 02-Jul-2001
CLASSIFICATION: <Unknown>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             COUNTRY: USA
ZIP: 20850
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
MOLECULE TYPE:
                                                                                                                                                                               TELECOMMUNICATION INFORMATION: TELEPHONE: 301-251-6015
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         CORRESPONDENCE ADDRESS:
ADDRESSEE: Human Genome Sciences, Inc
STREET: 9410 Key West Ave.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     NUMBER OF SEQUENCES: 12
                     STRANDEDNESS: single TOPOLOGY: linear
                                                                  TYPE: amino acid
                                                                                                                                                        TELEFAX: 301-309-8439
                                                                                                                                                                                                                             REFERENCE/DOCKET NUMBER: PF140
                                                                                                                                                                                                                                                  REGISTRATION NUMBER: 41,119
                                                                                                                                                                                                                                                                            NAME: Jonathan L. Klein
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Best Local 9
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LENGTH: 303
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Patent No. 6376226
GENERAL INFORMATION:
                                                                                                                                                                                                                                         Matches
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APPLICANT: Alhemi, Emad S.

TITLE OF INVENTION: RECOMBINANT, ACTIVE CASPASES AND USES

TITLE OF INVENTION: THEREOF

FILE REFERENCE: 480140.431

CURRENT APPLICATION NUMBER: US/09/561,756

CURRENT FILING DATE: 2000-04-26

PRIOR APPLICATION NUMBER: 09/227,721

PRIOR FILING DATE: 1999-01-08

NUMBER OF SEQ ID NOS: 116

NUMBER OF SEQ ID NOS: 116
                                                                                                                                                                                                                                                                                                LENGTH: 30
TYPE: PRT
                                                                                                                                                                                                                                                                                       ORGANISM: Homo sapien
301
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                                  FVQALCSILEEHGKDLEIMQILTRVNDRVARHFESQSDDPHFHEKKQIPCVVSMLTKELY
                                            FVQALCSILEEHGKELEIMQILTRVNDRVARHFESQSDDPHFHEKKQIPCVVSMLTKELY 300
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                                                                                                                                                                                                                                             99.6%;
99.3%;
                                                                                                                                                                                                                                   Score 1606; DB 4;
Pred. No. 6.4e-174;
1; Mismatches 1;
                                                                                                                                                                                                                                                       Length 303;
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GENERAL INFORMATION:
APPLICANT: Alnemri, Emad S.
TITLE OF INVENTION: RECOMBINANT, ACTIVE CASE
TITLE OF INVENTION: THEREOF
FILE REFERENCE: 480140.431
CURRENT APPLICATION NUMBER: US/09/227,721
CURRENT FILING DATE: 1999-01-08
NUMBER OF SEQ ID NOS: 116
SOFTWARE: FASTSEQ for Windows Version 3.0
SEQ ID NO 24
SEQ ID NO 24
                                                                                                                                                                                                                                                                                                RESULT 4
US-08-556-627A-2
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; ORGANISM: Homo
US-09-227-721-24
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US-09-227-721-24
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Patent No. 6379950
                                                                                                                                                                                                                               GENERAL INFORMATION:
APPLICANT: Alnemr
APPLICANT: Fernan
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Best Local Similarity
                                                                                                                          APPLICANT: Armstrong, Robert
APPLICANT: Tomaselli, Kevin
TITLE OF INVENTION: Mch3, A No. 6462175el A
TITLE OF INVENTION: Nucleic Acids Encoding
NUMBER OF SEQUENCES: 11
CORRESPONDENCE ADDRESS:
ADDRESSEE: Campbell and Flores
                                                COMPUTER READABLE FORM:
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          MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                     STREET: 4370 La
CITY: San Diego
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milarity 99.3%;
Conservative
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 PatentIn Release #1.0,
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RECOMBINANT, ACTIVE CASPASES
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Pred. No. 6.4e-174;
1; Mismatches 1;
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Matches
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Patent No. US20020076793A1
GENERAL INFORMATION:
APPLICANT: He, Wei-Wu et al.
TITLE OF INVENTION: Interleukin-1 Beta Converting Enzyme
                                                                                                                                                                                                                                                                                                                   Query Match
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INFORMATION FOR SEQ ID NO: 4:
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                                                                                                                                                                                                                                                                                             Local Similarity
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 APPLICATION NUMBER: <Unknown>
FILING DATE: <Unknown>
ATTORNEY/AGENT INFORMATION:
NAME: Jonathan L. Klein
                                                                                                                                                                                                                                                                                                                                                                            SEQUENCE DESCRIPTION: SEQ ID NO: 4:
                                                                                                                                                                                                                                                                                                                                                                                           MOLECULE TYPE: protein
                                                                                                                                                                                                                                                                                                                                                                                                                                                                        SEQUENCE CHARACTERISTICS:
LENGTH: 277 amino acids
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              SOFTWARE: PatentIn Release #1.0, Version #1.30 CURRENT APPLICATION DATA:
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ADDRESSEE: Human Genome Sciences,
STREET: 9410 Key West Ave.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
                                                                                                                NUMBER OF SEQUENCES:
                                      CVLLSHGEEGIIFGTNGPVDLKKITNFFRGDRCRSLTGKPKLFIIQACRGTELDCGIETD
                                                               CILLSHGEENVIYGKDGVTPIKDLTAHFRGDRCKTLLEKPKLFFIQACRGTELDDAIQAD 198
SGPINDTDANPRYKIPVEADFLFAYSTVPGYYSWRSPGRGSWFVQALCSILEEHGKELEI
                                                                                                                                                      DKVTGMGVRNGTDKDAEALFKCFRSLGFDVIVYNDCSCAKMQDLLKKASEEDHTNAACFA 138
                                                                                                                                                                                             ENSVDSKSIK-NLEPKIIHGSESMDSGISLDNS-----YKMDYPEMGLCIIINNKNF
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  COMPUTER: IBM PC compatible OPERATING SYSTEM: PC-DOS/MS-DOS
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US-10-103-448-3
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; ORGANISM: Homo sapien US-10-103-448-3
                                                                                                                                                                                                                                                                                                                    Sequence 3, Application US/10103448 Patent No. US20020155579A1 GENERAL INFORMATION:
                                                                             SEQ ID NO 3
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TITLE OF INVENTION: RECOMBINANT, ACTIVE CASPASES
TITLE OF INVENTION: THEREOF
                                                                                              NUMBER OF SEQ ID N
SOFTWARE: FastSEQ
                                                                                                                                                                         APPLICANT: Fritz, Lawrence C.
APPLICANT: Wu, JOSEPH C.
TITLE OF INVENTION: MEMBRANE DERIVED CASPASE-3,
TITLE OF INVENTION: COMPRISING THE SAME AND ME
FILE REFERENCE: 480140.46801
                                                                                                                                                                                                                                          APPLICANT: Krebs, Joseph F.
APPLICANT: Srinivasan, Anu
APPLICANT: Fritz, Lawrence
APPLICANT: Wu, Joseph C.
                                                                                                                                      CURRENT APPLICATION NUMBER: US/10/103,448
CURRENT FILING DATE: 2002-03-20
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                                     LENGTH: 264
TYPE: PRT
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Best Local Similarity
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TELEFAX: 30
INFORMATION FOR
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SEQUENCE CHARACTERISTICS:
REFERENCE/DOCKET NUMBER: 36,373
TELECOMMUNICATION INFORMATION:
TELEPHONE: 301-309-8504
TELEPAX: 301-309-8439
FORMATION FOR CO.
                                                                                                                                                                                                                          SOFTWARE: Patentin Release #1.0, Version #1.30 CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                               COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                           APPLICATION NUMBER: US 08 FILING DATE: 11-NOV-1994 ATTORNEY/AGENT INFORMATION: NAME: Brookes, A. Anders
                                                                                                                                                               CLASSIFICATION: 514
PRIOR APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                   APPLICANT: He, Wei-Wu et al.
TITLE OF INVENTION: Interleu
TITLE OF INVENTION: Like Apo
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CTTY: Rockville
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STRANDEDNESS: single
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05-JUN-1995
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                                                                                                                                                US 08/334,251
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Best Local Similarity
Matches 144; Conserv
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                                                                 PRIOR APPLICATION DATA:
APPLICATION NUMBER: 60/030,408
FILING DATE: 04-NOV-1996
APPLICATION NUMBER: PCT/CA97/00825
FILING DATE: 03 -NOV-1996
                                                                                                                                                                                   COMPUTER: IBM Compatible
OPERATING SYSTEM: DOS
SOFTWARE: FastSEQ for Windows Version
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/964,313
FILING DATE: 04-NOV-1997
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                                                  FILING DATE: 03 -NOV-199 ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                             COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette
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LENGTH: 277 amino acids
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REFERENCE/DOCKET NUMBER: 19824Y
             NAME: DURETTE, PHILIPPE L. REGISTRATION NUMBER: 35,125
                                                                                                                                                                  CLASSIFICATION:
                                                                                                                                                                                                                                                                                                                                                   COUNTRY:
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04-NOV-1997
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; Pred. No. 1.6e-73;
50; Mismatches 77;
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// ORGANISM: Homo sapien
US-09-954-697-33
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                GENERAL INFORMATION:
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                                                                     PRIOR APPLICATION NUMBER: PCT/EP98/01857
PRIOR FILING DATE: 1998-03-31
PRIOR APPLICATION NUMBER: GERMANY 197 13 393.2
PRIOR FILING DATE: 1997-04-01
                                                                                                                                                                                                                                     CURRENT APPLICATION NUMBER: US/09/410,194
CURRENT FILING DATE: 1999-09-30
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SOFTWARE: FastSEQ for Windows Version 4.0
                                                                                                                                                                                                                                                                                                       APPLICANT: Hofmann, Kay
APPLICANT: French, E. Lars
TITLE OF INVENTION: FLIP GENES AND FLIP PROTEINS
FILE REFERENCE: 11141-002001
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Pred. No. 1.5e-37;
8; Mismatches 109
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; ORGANISM: Homo sapiens US-09-410-194-21
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LENGTH: 571
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                                                                                                                                                                                                                                             CURRENT APPLICATION NUMBER: US/09/410,194
CURRENT FILING DATE: 199-09-30
PRIOR APPLICATION NUMBER: PCT/EP98/01857
PRIOR FILING DATE: 1998-03-31
                                                                                                                                                                       SOFTWARE: FastSEQ for Windows Version 4.0
                                                                                                                                                                                                                                                                                                                       APPLICANT: Hofmann, Kay
APPLICANT: French, E. Lars
TITLE OF INVENTION: FLIP GENES AND FLIP PROTEINS
FILE REFERENCE: 11141-002001
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o. US20020095030A1
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61;
                 Score 425.5; DB 10; Pred. No. 1.7e-35;
 Mismatches 110;
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                                                                                                   APPLICANT: David WALLACH
APPLICANT: David WALLACH
APPLICANT: Mark P. BOLDIN
APPLICANT: Mark P. BOLDIN
APPLICANT: Tanya M. GONCHAROV
APPLICANT: Yury V. GOLTSEV
APPLICANT: YURY V. GOLTSEV
APPLICANT: YURY V. GOLTSEV
APPLICANT: YURY V. GOLTSEV
APPLICANT: OTHER PROTEINS
                                                                                                                                                                                                                                                  Sequence 30, Application US/08983502 Patent No. 6399327
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Query Match
Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Sequence 12, Application US/09227721
Patent No. 6379950
GENERAL INFORMATION:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          TITLE OF INVENTION: RECOMBINANT, ACTIVE CASPASES AND USES TITLE OF INVENTION: THEREOF FILE REFERENCE: 480140.431
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     NUMBER OF SEQ ID NOS: 116
SOFTWARE: FastSEQ for Windows Version 3.0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           CURRENT APPLICATION NUMBER: US/09/227,721 CURRENT FILING DATE: 1999-01-08
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    APPLICANT: Alnemri, Emad S.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      TYPE: PRT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       LENGTH:
                                                                                    TITLE OF INVENTION: MODULATORS OF THE TITLE OF INVENTION: AND OTHER PROTEINS NUMBER OF SEQUENCES: 34
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                 233
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 79 DKVTGMGVRNGTDKDAEALFKCFRSLGFDVIVYNDCSCAKMQDLLKKASEEDHTNAACFA 138
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 19 EDSVDAKPDRSSFVPSLFSKKKKNVTMRSIKTTRDRVPTYQYNMNFEKLGKCIIINNKNF 78
 COUNTRY:
                                                  STREET: 419 Seventh Street N.W.,
                                                                      ADDRESSEE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               S ENSVDSKSIK-NLEPKIIHGSESMDSGISLDNS-----YKMDYPEMGLCIIINNKNF
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                                                                                                                                                                                                                                                                                                                                                                            MQILTRVNDRVARHFESQSDDPHFHEKKQIPCVVSMLTKELYF 301
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     CILLSHGEENVIYGKDGVTPIKDLTAHFRGDRCKTLLEKPKLFFIQACRGTELDDAIQAD
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                  Washington D.C.
USA
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                                                                      Browdy and Neimark
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Best Local Similarity 50.5%;
Matches 143; Conservative 5
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INFORMATION FOR SEQ ID NO:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          NAME: Browdy, Roger L.
REGISTRATION NUMBER: 25,618
REFERENCE/DOCKET NUMBER: WAI
TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 PRIOR APPLICATION DATA:
APPLICATION NUMBER: IL 117,932
FILING DATE: 16-APR-1996
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            TOPOLOGY: linear MOLECULE TYPE: protein
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PRIOR APPLICATION DATA:
11 115,319
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APPLICATION NUMBER: IL 114,986
FILING DATE: 17-AUG-1995
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FILING DATE: 14-JUN-1996
PRIOR APPLICATION DATA:
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233 MHILTRVNRKVATEFESFSFDATFHAKKQIPCIVSMLTKELYF
                                    259 MQILTRVNDRVARHFESQSDDPHFHEKKQIPCVVSMLTKELYF 301
                                                                                                                                                                               139 CILLSHGEENVIYGKDGVTPIKDLTAHFRGDRCKTLLEKPKLFFIQACRGTELDDAIQAD 198
                                                                                                                  199 SGPINDTDANPRYKIPVEADFLFAYSTVPGYYSWRSPGRGSWFVQALCSILEEHGKELEI
                                                                                                                                                        116 CVLLSHGEEGIIFGTNGPVDLKKITNFFRGDRCRSLTGKPKLFIIQACRGTELDCGIETD
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                                                                                                                                                                                                                                                            79 DKVTGMGVRNGTDKDAEALFKCFRSLGFDVIVYNDCSCAKMQDLLKKASEEDHTNAACFA 138
                                                                                                                                                                                                                                                                                                                                                        19 EDSVDAKPDRSSFVPSLFSKKKKNVTMRSIKTTRDRVPTYQYNMNFEKLGKCIIINNKNF 78
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OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
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                                                                             SGVDDDMAC---HKIPVDADFLYAYSTAPGYYSWRNSKDGSWFIQSLCAMLKQYADKLEF
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16-JUL-1995
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                                                                                                                                                                                                                                                                                                                                                                                               Score 718; DB 4; Length 277; Pred. No. 3.5e-73; Indels
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RESULT 13 PCT-US96-10521-30

Sequence 30, Application PC/TUS9610521 GENERAL INFORMATION:

APPLICANT

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FILE REFERENCE: 480140.431D2
CURRENT APPLICATION NUMBER: US/09/954,697
CURRENT FILING DATE: 2001-09-14
NUMBER OF SEQ ID NOS: 116
SOFTWARE: FastSEQ for Windows Version 3.0
SEQ ID NO 27
LENGTH: 476
TYPE: PRT
ORGANISM: Homo sapien
US-09-954-697-27
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Best Local Similarity 37.4
Description 98; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         APPLICANT: Alnemri, Emad S.
TITLE OF INVENTION: RECOMBINANT, ACTIVE CASPASES
TITLE OF INVENTION: THEREOF
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            452 DKKNMGKQMPQPTFTLRKKLVF 473
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   172 KTLLEKPKLFFIQACRGTELDDAIQADSGPINDTDANP-----RYKIPVEADEL 220
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     398 LGMATVNNCVSYRNPAEGTWYIQSLCQSLRERCPRGDDILTILTEVN---
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             60 YNMNFEKLGKCIIINNKNF-----DKVTGMGVRNGTDKDAEALFKCFRSLGFDVIVYN 112
                                                                                                                                                                   COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOPTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/962,834A
FILING DATE: 25-Sep-2001
CLASSIFICATION: <Unknown>
PRIOR APPLICATION DATA:
REFERENCE/DOCKET NUMBER: G15276
TELECOMMUNICATION INFORMATION:
TELEPHONE: (617) 498-8224
                                                                                                                                                                                                                                                                                                                                       COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       TITLE OF INVENTION: NOVEL PROTEASE NUMBER OF SEQUENCES: 2
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                                                                                                       ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 APPLICANT: Bowman, Michael
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                                                                                                                                                                                                                                                                                                                                                                                     COUNTRY: USA
ZIP: 02140
                                                                                                                                                                                                                                                                                                                                                                                                                                                   STREET: 87 Camb:
CITY: Cambridge
                                                           NAME: Brown, Scott A. REGISTRATION NUMBER: 32,724
                                                                                                                           APPLICATION NUMBER: 08/675,123 FILING DATE: 1996-07-03
                                                                                                                                                                                                                                                                                                                                                                                                                               STATE: Massachusetts
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ADDRESSEE: Genetics Institute, Inc
                                                                                                                                                                                                                                                                                                                                                                                                                                                                     87 CambridgePark Drive
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Pred. No. 4.4e~35;
3; Mismatches 90;
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Search completed: December Job time: 9.35862 secs

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                                                                        444
469
                                                                                                                                                384
                                                                                                                                                                                     169
                                                                                                                                                                                                                          324
                                 287 QIPCVVSMLTKEL 299
                                                                                                             227
                                                                                                                                                                                                                                                           111 YNDCSCAKMODLLKKAS-EEDHTNAACFACILLSHGEENVIYGKD-GVTPIKDLTAHFRG 168
                                                                                                                                                                                                                                                                                                                                                                            209 QGEEELVSQTDVKTFLEALPQESWQNKHAGSNGNRATNGAPSLVSRGMQGASANTLNSET 268
                                                                                                                                                                                                                                                                                                   269 STKRAAVYRMNRNHR--GLCVIVNNHSF---TSLKDRQGTHKDAEILSHVFQWLGFTVHI 323
                                                                                                                                                                                                                                                                                                                                                                                                               11 QGVEDSANEDSV----DAKPDRS----
                                                                                                                                                                                                                                                                                                                                     51 TRDRVPTYQYNMNFEKLGKCIIINNKNFDKVTGMGVRNGTDKDAEALFKCFRSLGFDVIV 110
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   TOPOLOGY:
                                                                                                                                                                                 DRCKTLLEKPKLFFIQACRGTELDDAIQADSGPINDTDA--NPRYKIPVEADFLFAYSTV 226
                                                                                                                                                                                                                        HNNVTKVEMEMYLQKQKCNPAHADGDCFVFCILTHGRFGAVYSSDEALIPIREIMSHFTA 383
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 SEQUENCE DESCRIPTION: SEQ ID NO: 2:
LVPRMLKFLEKTM 481
                                                                                                                                                LOCPRLAEKPKLFFIQACQGEEIQPSVSIEADALNPEQAPTSLQDSIPAEADFLLGLATV 443
                                                                        PGYVSFRHVEEGSWYIQSLCN---
                                                                                                           PGYYSWRSPGRGSWFVQALCSILEEHGKELEIMQILTRVNDRVARHFESQSDDPHFHEKK 286
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       LENGTH: 521 amino acids TYPE: amino acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       STRANDEDNESS: <Unknown>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     TELEFAX: (617) 876-5851
                                                                                                                                                                                                                                                                                                                                                                                                                                                     Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   protein
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30.4%;
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Pred. No. 2e-32;
                                                                                                                                                                                                                                                                                                                                                                                                                                                     Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                 -----SFVPSLFSKKKKNVTMRSI--KT 50
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       DB 10; Length 521;
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INFORMATION FOR SEQ ID NO: 10
SEQUENCE CHARACTERISTICS:
ENGTH: 277 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: peptide
US-08-964-313-10
Search completed: December Job time: 16.1052 secs
                                                                                                                                                                                                                                                                                                                                                                                           Query Match
Best Local Similarity
Matches 143; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                PRIOR APPLICATION: 435
PRIOR APPLICATION NUMBER: 60/030,408
FILING DATE: 04-NOV-1996
APPLICATION NUMBER: PCT/CA97/00825
FILING DATE: 03-NOV-1996
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         NAME: DURETTE, PHILIPPE L. REGISTRATION NUMBER: 35,125. REFERENCE/DOCKET NUMBER: 19824Y TELECOMMUNICATION INFORMATION: 732-594-4568
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette
COMPUTER: IBM COMPATIL
OPERATING SYSTEM: DOS
                                                         OPERATING SYSTEM: DOS
SOFTWARE: FastSEQ for Windows Version 2.0
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/964,313
FILING DATE: 04-NOV-1997
                                                                                                                                                                                        ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                        COUNTRY: US.
ZIP: 07065
                                                                                                                                                                                                                                                        56 HKSTGMTSRSGTDVDAANLRETFRNLKYEVRNKNDLTREEIVELMRDVSKEDHSKRSSFV 115
                                                                                                                                                                                                                                                                          79 DKVTGMGVRNGTDKDAEALFKCFRSLGFDVIVYNDCSCAKMQDLLKKASEEDHTNAACFA 138
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            TELEPHONE: 732-594-4720
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ADDRESSEE: PHILIPPE L. DURETTE - MERCK & CO., INC. STREET: 126 EAST LINCOLN AVENUE - P.O. BOX 2000 CITY: RAHWAY
                                                                                                                                                                                                                                                                                                                                                                                             Conservative
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               2002, 12:58:44
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Result
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Maximum Match 100%
Listing first 45 summaries
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Maximum DB seq
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1: /cgn2_6/ptodata/1/
2: /cgn2_6/ptodata/1/
3: /cgn2_6/ptodata/1/
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            length: 2000000000
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                                                                                                                                                                                                                                                                                                                                                                                                                                                         /cgn2_6/ptodata/1/laa/5A_COMB.pep:*
/cgn2_6/ptodata/1/laa/5A_COMB.pep:*
/cgn2_6/ptodata/1/laa/6A_COMB.pep:*
/cgn2_6/ptodata/1/laa/6B_COMB.pep:*
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DB
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      US-08-964-308-6
US-08-964-313-6
US-09-964-313-6
US-09-961-756-12
US-09-961-756-12
US-09-961-308-10
US-08-98-3-502-30
US-08-98-3-502-30
US-08-964-313-10
US-08-964-313-10
US-08-964-313-10
US-08-964-313-10
US-08-964-313-10
US-08-964-313-10
US-08-964-313-10
US-08-913-6088-2
US-08-913-6088-2
US-08-913-5
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US-08-591-605-2
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632.048 Million cell updates/sec
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423.5	423.5	424.5	424.5	424.5	424.5	424.5	424.5	424.5	425.5	425.5	426.5	444.5	444.5	444.5	444.5	444.5	466
26.3	26.3	26.3	26.3	26.3	26.3	26.3	26.3	26.3	26.4	26.4	26.4	27.6	27.6	27.6	27.6	27.6	28.9
389	286	479	479	479	479	479	479	479	479	479	479	479	479	479	479	346	293
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US-08-618-408B-4	US-09-360-017-1	US-09-074-044A-28	US-09-074-044A-27	US-09-074-044A-26	US-09-001-777-12	US-09-382-155-28	US-09-382-155-26	US-08-807-200-12	PCT-US96-10521-7	US-08-983-502-7	US-09-382-155-27	US-09-227-721-33	US-09-561-756-33	US-09-291-692-2	US-08-665-220-2	US-08-618-408B-2	PCT-US96-10521-31
Sequence 4, Appli	Sequence 1, Appli	Sequence 28, Appl	Sequence 27, Appl	26,	12	28,		12,	Sequence 7, Appli	7,	27,	ω	Sequence 33, Appl	2	Sequence 2, Appli	~	Sequence 31, Appl

ALIGNMENTS

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US-08-462-969B-2
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US-08-462-969B-2
                  Query Match
Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Sequence 2, Application US/08462969B Patent No. 6087150
                                                                                                                                                                                      TELEFAX: 301-309-8439 INFORMATION FOR SEQ ID NO:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         GENERAL INFORMATION: APPLICANT: He, We
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ZIP: 20850
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy
                                                                                    TOPOLOGY: 1: MOLECULE TYPE:
                                                                                                                                                                                                   REFERENCE/DOCKET NUMBER: PF
TELECOMMUNICATION INFORMATION:
TELEPHONE: 301-309-8504
TELEFAX: 301-309-8439
                                                                                                                                                                                                                                                                                        FILING DATE: 11-NOV-1994
ATTORNEY/AGENT INFORMATION:
NAME: Brookes, A. Anders
                                                                                                                                                                                                                                                                                                                                   PRIOR APPLICATION DATA:
APPLICATION NUMBER:
                                                                                                                                                                                                                                                                                                                                                                                      SOFTWARE: PatentIn Release #1.0, V
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/462,969B
FILING DATE: 05-JUN-1995
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              CILL NL STATE: NL COUNTRY: USA TTD: 20850
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   APPLICANT: He, Wei-Wu et al.
TITLE OF INVENTION: Interleu
TITLE OF INVENTION: Like Apo
NUMBER OF SEQUENCES: 12
                                                                                                                                                                    SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                  COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ADDRESSEE: Human Genome Sciences, Inc. STREET: 9410 Key West Ave. CITY: Rockville
                                                                                                                    STRANDEDNESS:
                                                                                                                                                                                                                                                                      NAME: Brookes, A. Anders REGISTRATION NUMBER: 36,
                                                                                                                                                   LENGTH:
                                                                                                                                  amino acid
                                                                                                                                                       303
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                                                                                                   SS: single
linear
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                                                                                                                                                     amino acids
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Score 1613; DB 3;
Pred. No. 1e-174;
); Mismatches 0;
                                  Length 303;
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Matches

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APPLICANT: Alnemri, Emad S.
TITLE OF INVENTION: RECOMBINANT, ACTIVE CASPASES AND USES
TITLE OF INVENTION: THEREOF
FILE REFERENCE: 480140.431
CURRENT EPLICATION NUMBER: US/09/561,756
CURRENT FILING DATE: 2000-04-26
CURRENT FILING DATE: 7000-04-26
                                                                                                                                                                                                                                                                                       Query Match
Best Local Similarity
                                                                                                                                                                                                                                                                                Matches
                                                                                                                                                                                                                                                                                                                                                             SEQ ID NO 24
LENGTH: 303
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Sequence 24, Application US/09561756 Patent No. 6376226
                                                                                                                                                                                                                                                                                                                                                                                   SOFTWARE: FastSEQ for Windows Version
                                                                                                                                                                                                                                                                                                                                                                                              PRIOR APPLICATION NUMBER: 09/227,721
PRIOR FILING DATE: 1999-01-08
NUMBER OF SEQ ID NOS: 116
                                                                                                                                                                                                                                                                                                                                                     TYPE: PRT
 301
                       301
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                                                                                                                                 FFIQACRGTELDDAIQADSGPINDTDANPRYKIPVEADFLFAYSTVPGYYSWRSPGRGSW
                                                                                                                                                                               NMNFEKLGKCIIINNKNFDKVTGMGVRNGTDKDAEALFKCFRSLGFDVIVYNDCSCAKMQ
FSQ 303
                       FSQ 303
                                                                                     FFIQACRGTELDDGIQADSGPINDTDANPRYKIPVEADFLFAYSTVPGYYSWRSPGRGSW
                                                                                                                                                                                          NMNFEKLGKCIIINNKNEDKYTGMGVRNGTDKDAEALFKCFRSLGFDVIVYNDCSCAKMQ
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             FFIQACRGTELDDAIQADSGPINDTDANPRYKIPVEADFLFAYSTVPGYYSWRSPGRGSW
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                                                                                                                                                                                                                                                                            301;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       DLLKKASEEDHTNAACFACILLSHGEENVIYGKDGVTPIKDLTAHFRGDRCKTLLEKPKL 180
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      MADDQGCIEEQGVEDSANEDSVDAKPDRSSFVPSLFSKKKKNVTMRSIKTTRDRVPTYQY
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                                                                                                                                                                                                                                                                                     99.6%;
                                                                                                                                                                                                                                                                                    Score 1606; DB 4;
Pred. No. 6.4e-174;
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US-09-227-721-24
                                                                                                                                                                                                                                                Patent No. 6462175
GENERAL INFORMATION:
                                                                                                                                                                                                                                                                         Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Query Match
Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              NUMBER OF SEQ ID NOS: 116
SOFTWARE: FastSEQ for Windows Version 3.0
SEQ ID NO 24
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            GENERAL INFORMATION:
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TITLE OF INVENTION: RECOMBINANT, ACTIVE CITITLE OF INVENTION: THEREOF
FILE REFERENCE: 480140.431
CURRENT APPLICATION NUMBER: US/09/227,721
CURRENT FILING DATE: 1999-01-08
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Sequence 24, Application US/09227721 Patent No. 6379950
ZIP: 92122
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          LENGTH: 3C
                                                                                                                                                           APPLICANT: Armstrong, Robert APPLICANT: Tomaselli, Kevin TITLE OF INVENTION: Mch3, A TITLE OF INVENTION: Nucleic
                                                                                                                                       NUMBER OF SEQUENCES: 1
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                         APPLICANT:
APPLICANT:
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                                                                             COUNTRY:
                                                                                                   STREET: 4370 La
CITY: San Diego
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                                                                                                                           ADDRESSEE:
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                                                                                         California
                                                                                                               E: Campbell and Flores
4370 La Jolla Village Drive, Suite 700
                                                                              USA
                                                                                                                                                                                                                         Fernandes-Alnemri,
                                                                                                                                                                                                               Litwack, Gerald
                                                                                                                                                                                                                                       Alnemri,
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Pred. No. 6.4e-174;
1; Mismatches 1;
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ds Encoding and Methods of Use
     Version
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Patent No. 6060238
GENERAL INFORMATION:
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ATTORNEY/AGENT INFORMATION:
NAME: Campbell, Cathryn A.
REGISTRATION UNUMBER: 31,815
REFERENCE/DOCKET NUMBER: P-ID
TELEPHONE: (619) 535-9001
TELEPHONE: (619) 535-9001
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                TELEFAX: (619) 535-8949 INFORMATION FOR SEQ ID NO:
         SOFTWARE: PatentIn Release #1.0, CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/591,605
FILING DATE: 09-FEB-1996
                                                                       COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                               CORRESPONDENCE ADDRESS:
ADDRESSEE: MORRISON & FOERSTER
STREET: 755 PAGE MILL ROAD
                                                                                                                                                                                                                                                              TITLE OF INVENTION:
                                                                                                                                                                                                                                                                 APPLICANT: Dixit, Vishva M.
APPLICANT: Dixit, Vishva M.
TITLE OF INVENTION: METHOD AND COMPOSITION FOR REGULATING
                                                                                                                                                                                                                                                 NUMBER OF SEQUENCES:
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TOPOLOGY: linear
MOLECULE TYPE: prot
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                                                                                                                                                                             STREET: 755 PAGE
CITY: PALO ALTO
CLASSIFICATION:
                                                                                                                                    COUNTRY: USA
ZIP: 94304-1018
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                                                        PatentIn Release #1.0, Version #1.30
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99.3%;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Patent No. 6066715
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Best Local Similarity
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TELEFAX: (415) 494-0792
TELEX: 706141 MRSNFOERS SFO
INFORMATION FOR SEQ ID NO: 2:
                                                                                                COMPUTER: IBM PC Compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Fast-SEQ for Windows Version
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/964,308
FILLING DATE: 04-NOV-1996
CLASSIFICATION: 530
                                ATTORNEY/AGENT INFORMATION:
NAME: NORTH, ROBERT J
REGISTRATION NUMBER: 27,
                                                                                                                                                                                                                                                                                                                                                                                                                                               APPLICANT: DESMARAIS, SYLVIE
APPLICANT: FRIESEN, RICHARD
APPLICANT: ZAMBONI, ROBERT
TITLE OF INVENTION: NEW LIGANDS FOR PHOSPHATASE
TITLE OF INVENTION: BINDING ASSAY
                                                                                                                                                                                                                                             COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy 1
                                                                                                                                                                                                                                                                                                                                                                                                                                TITLE OF INVENTION:
TITLE OF INVENTION:
NUMBER OF SEQUENCES:
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REFERENCE/DOCKET NUMBER: 20
TELECOMMUNICATION INFORMATION:
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LENGTH: 277 amino acids
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REFERENCE/DOCKET NUMBER: 198
                                                                                                                                                                                                                                                                                        COUNTRY: UZIP: 07065
                                                                                                                                                                                                                                                                                                                                STATE:
                                                                                                                                                                                                                                                                                                                                                   CITY: RAHWAY
                                                                                                                                                                                                                                                                                                                                                                  ADDRESSEE: ROBERT J. NORTH - MERCK & CO., INC. STREET: 126 EAST LINCOLN AVENUE - P.O. BOX 2000
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    56 HKSTGMTSRSGTDVDAANLRETFRNLKYEVRNKNDLTREEIVELMRDVSKEDHSKRSSFV 115
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             79 DKVTGMGVRNGTDKDAEALFKCFRSLGFDVIVYNDCSCAKMQDLLKKASEEDHTNAACFA 138
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   TYPE: amino acid
TOPOLOGY: linear
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                                                                                                                                                                                                                                                                                                           USA
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                                                                                                                                                                                                                                             Floppy Diskette
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50.9%; Pred. No. 1
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Pred. No. 1.6e-73;
Pred. no. 1.6e-73;
                   9840 PCT
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RESULT 7
US-08-462-969B-4
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Best Local Similarity
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INFORMATION FOR SEQ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                               GENERAL INFORMATION: APPLICANT: He, We
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                                                                                                                    APPLICATION NUMBER: US/08/462,969E
FILING DATE: 05-JUN-1995
CLASSIFICATION: 514
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/334,251
FILING DATE: 11-NOV-1994
                                                                                                                                                                                                             COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
                                                                                                       FILING DATE: 11-NOV-1994
ATTORNEY/AGENT INFORMATION:
                                          TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                               NUMBER OF SEQUENCES: 1
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                           APPLICANT: He, Wei-Wu et al
TITLE OF INVENTION: Interle
TITLE OF INVENTION: Like App
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LENGTH: 277 amino acid
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                                                                                                                                                                                                                                                                                                                                                    STREET: >***
              TELEPHONE: 301-309-8504
TELEFAX: 301-309-8439
                                                            REFERENCE/DOCKET NUMBER:
                                                                             REGISTRATION NUMBER:
                                                                                             NAME:
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TYPE: amino acid
STRANDEDNESS: si
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732-594-4720
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Like Apoptosis Protease 3 and
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Sequence 6,
         APPLICATION NUMBER: 60/030,408
FILING DATE: 04-NOV-1996
APPLICATION NUMBER: PCT/CA97/00825
FILING DATE: 03-NOV-1996
ATTORNEY/AGENT INFORMATION:
NAME: DURETTE, PHILIPPE L.
REGISTRATION NUMBER: 35,125
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Matches 144; Conserv
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Best Local S
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                                                                                                                                                                                      SOFTWARE: FastSEQ for Windows Version CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                   COMPUTER READABLE FORM: MEDIUM TYPE: Diskett
                                                                                                                         CLASSIFICATION: 435
PRIOR APPLICATION DATA:
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                                                                                                                                                                                                                                                                                                                                                                                                     NUMBER OF SEQUENCES:
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                                                                                                                                                                                                                COMPUTER: IBM CON
OPERATING SYSTEM:
REGISTRATION NUMBER: 35,125
                                                                                                                                                        FILING DATE: 04-NOV-1997
                                                                                                                                                                         APPLICATION NUMBER:
                                                                                                                                                                                                                                                                                                   COUNTRY:
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STRANDEDNESS: sir
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RAMACHANDRAN, CHIDAMBARAN
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IBM Compatible
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50.9%; Pred. No. 1.6e-73;
... Mismatches 77;
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GENERAL INFORMATION:
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy Diskette
COMPUTER: IBM PC Compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: FASTSEQ for Windows Version 2.
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/069,138
FILING DATE: 29-APR-1998
CLASSIFICATION: 530
ATTORNEY/AGENT INFORMATION:
NAME: DURETTE, PHILIPPE L.
REGISTRATION NUMBER: 35,125
REFERENCE/DOCKET NUMBER: 19840YIA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Matches 144;
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Best Local 9
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                                                                                                                                                                                                                                                                                                   CORRESPONDENCE ADDRESS:
ADDRESSEE: PHILIPPE L. DURETTE • MERCK & CO., I
STREET: 126 EAST LINCOLN AVENUE - P.O. BOX 2000
                                                                                                                                                                                                                                                                                                                                                          APPLICANT: ZAMBONI, ROBERT
TITLE OF INVENTION: NEW LIGANDS FOR PHOSPHATASE
TITLE OF INVENTION: BINDING ASSAY
NUMBER OF SEQUENCES: 15
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                                                                                                                                                                                                                                                                        CITY: RAHWAY
STATE: NJ
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TELEFAX: 732-594-4720
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LEBLANC, YVES
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; Pred. No. 1.6e-73;
; wismatches 77;
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PRIOR TILING DATE: 2000-04-26
PRIOR APPLICATION NUMBER: 09/227,721
PRIOR FILING DATE: 1999-01-08
NUMBER OF SEQ ID NOS: 116
SOFTWARE: FastSEQ for Windows Version 3.0
SEO ID NO 12
LENGTH: 277
TYPPE: 7577
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APPLICANT: Alnemri, Emad S.
TITLE OF INVENTION: RECOMBINANT, ACTIVE CASPASES AND USES
TITLE OF INVENTION: THEREOF
                                                                                                                                                                                                                   Matches 143;
                                                                                                                                                                                                                                                           Query Match
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Patent No. 6376226
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Best Local S
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                                                                                                                                                                                                                                                                                                                                       TYPE: PRT
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LENGTH: 277 amino acids
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139 CILLSHGEENVIYGKDGVTPIKDLTAHFRGDRCKTLLEKPKLFFIQACRGTELDDAIQAD 198
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                                                         56 HKSTGMTSRSGTDVDAANLRETFRNLKYEVRNKNDLTREEIVELMRDVSKEDHSKRSSFV 115
                                                                                                   79
                                                                                                                                                                       19 EDSVDAKPDRSSFVPSLFSKKKKNVTMRSIKTTRDRVPTYQYNMNFEKLGKCIIINNKNF 78
                                                                                                                                                                                                                                     Match 44.5%;
Local Similarity 50.5%;
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                                                                                             DKVTGMGVRNGTDKDAEALFKCFRSLGFDVIVYNDCSCAKMQDLLKKASEEDHTNAACFA 138
                                                                                                                                       ENSVDSKSIK-NLEPKIIHGSESMDSGISLDNS-----YKMDYPEMGLCIIINNKNF 55
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50.9%; Pred. No. 1.6e-73;
50.9%; Mismatches 77;
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                                                                                                                                                                                                             Score 718; DB 4; L
Pred. No. 3.5e-73;
Pred. No. 3.5e-77;
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RESULT 12
US-08-983-502-30
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US-09-227-721-12
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SOFTWARE: FastSEQ for Windows Version 3.0
SEQ ID NO 12
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APPLICANT: Alnemri, Emad S.
APPLICANT: Alnemri, Emad S.
TITLE OF INVENTION: TREREOF
TITLE OF INVENTION: THEREOF
                                                                                                                                                                                                                                    Sequence 30, Application US/08983502
Patent No. 6399327
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Matches
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TYPE: PRT
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                                                                                                                                                 APPLICANT:
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APPLICANT:
                                                                                                 TITLE OF INVENTION: MODULATORS OF THE FUNCTION OF FAS RECEPTORS TITLE OF INVENTION: AND OTHER PROTEINS NUMBER OF SEQUENCES: 34
                                                                                 CORRESPONDENCE ADDRESS:
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                               CITY:
                                               STREET:
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mes 143; Conserv
                                                               ADDRESSEE:
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                            Washington
                 D.C.
                                              419 Seventh Street N.W.,
                                                                                                                                                               Mark P. BOLDIN
Tanya M. GONCHAROV
                                                                                                                                                 Yury V. GOLTSEV
                                                                                                                                                                                                      David WALLACH
USA
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US-08-983-502-30
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Best Local
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INFORMATION FOR SEQ ID NO:
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LENGTH: 277 amino acids
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TELECOMMUNICATION INFORMATION:
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ATTORNEY/AGENT INFORMATION:
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APPLICATION NUMBER:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     CURRENT APPLICATION DATA:
233 MHILTRVNRKVATEFESFSFDATFHAKKQIPCIVSMLTKELYF 275
                                                                                                                                                  259 MOILTRVNDRVARHFESOSDDPHFHEKKQIPCVVSMLTKELYF 301
                                                                                                                                                                                       139 CILLSHGEENVIYGKDGVTPIKDLTAHFRGDRCKTLLEKPKLFFIQACRGTELDDAIQAD 198
                                                                                                                                                                                                                             56 HKSTGMTSRSGTDVDAANLRETFRNLKYEVRNKNDLTREEIVELMRDVSKEDHSKRSSFV 115
                                                                                                                                                                                                                                                                      79
                                                                                                                                                                                                                                                                                                                                         19 EDSYDAKPDRSSFYPSLFSKKKKNYTMRSIKTTRDRYPTYQYNMNFEKLGKCIIINNKNF 78
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     NAME: Browdy, Roger L.
REGISTRATION NUMBER: 25,618
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   APPLICATION NUMBER: FILING DATE: 16-JA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
                                                                                                                                                                                                                                                                                                                                                                                   Local Similarity 50.9 es 143; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           APPLICATION NUMBER: IL 116,588 FILING DATE: 27-DEC-1995
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          FILING DATE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                MEDIUM TYPE: Floppy
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            FILING DATE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             APPLICATION NUMBER:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              APPLICATION NUMBER: PCT/US96/1052
                                                                                                                                                                                                                                                                                                        5 ENSVDSKSIK-NLEPKIIHGSESMDSGISLDNS-----YKMDYPEMGLCIIINNKNF 55
                                                                                          SGPINDTDANPRYKIPVEADFLFAYSTVPGYYSWRSPGRGSWFVQALCSILEEHGKELEI 258
                                                                                                                                                                                                                                                              DKVTGMGVRNGTDKDAEALFKCFRSLGFDVIVYNDCSCAKMQDLLKKASEEDHTNAACFA 138
                                                                         SGVDDDMAC---HKIPVDADFLYAYSTAPGYYSWRNSKDGSWFIQSLCAMLKQYADKLEF
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       amino acid
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                737-3528
                                                                                                                                                                                                                                                                                                                                                                               44.5%; Score 718; DB 4; 1
50.5%; Pred. No. 3.5e-73;
7ative 51; Mismatches 77;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             IL 114,986
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RESULT 13 PCT-US96-10521-30

Sequence 30, Application GENERAL INFORMATION:

PC/TUS9610521

APPLICANT:

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US-08-964-308-10
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                                                                                                                                            Patent No.
                                                                                                                                              Sequence 10, Application US/08964308 Patent No. 6066715
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Best Local 9
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                                                                                                                            GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        FILING DATE: 16-APR-1996 INFORMATION FOR SEQ ID NO: 3
         APPLICANT: DESMARAIS, SYLVIE
APPLICANT: FRIESEN, RICHARD
APPLICANT: ZAMBONI, ROBERT
TITLE OF INVENTION: NEW LIGANDS FOR PHOSPHATASE
TITLE OF INVENTION: BINDING ASSAY
NUMBER OF SEQUENCES: 15
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  APPLICATION NUMBER:
FILING DATE: 14-SEP-
PRIOR APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           PRIOR APPLICATION DATA:
APPLICATION NUMBER: IL 115,319
FILING DATE: 14-SEP-1995
FILING DATE: 14-SEP-1995
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         APPLICATION NUMBER: IL 11
FILING DATE: 16-JUL-1995
PRIOR APPLICATION DATA:
APPLICATION NUMBER: IL 11
FILING DATE: 17-AUG-1995
CORRESPONDENCE ADDRESS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         MOLECULE TYPE: protein
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     SEQUENCE CHARACTERISTICS:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     CLASSIFICATION:
PRIOR APPLICATION DATA:
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mes 143; Conserv
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   FILING DATE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 COMPUTER: IBM PC compatible OPERATING SYSTEM: PC-DOS/MS-DOS
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               APPLICATION NUMBER: IL 1: FILING DATE: 27-DEC-1995
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                                                                                                                                                                                                                                                                                                                                                                                                                     CILLSHGEENVIYGKDGVTPIKDLTAHFRGDRCKTLLEKPKLFFIQACRGTELDDAIQAD 198
                                                                                                                                                                                                                                                                                                                                                                                                                                                                            HKSTGMTSRSGTDVDAANLRETFRNLKYEVRNKNDLTREEIVELMRDVSKEDHSKRSSFV 115
                                                                                                                                                                                                                                                                                                                            SGVDDDMAC---HKIPVDADFLYAYSTAPGYYSWRNSKDGSWFIQSLCAMLKQYADKLEF 232
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               DKVTGMGVRNGTDKDAEALFKCFRSLGFDVIVYNDCSCAKMQDLLKKASEEDHTNAACFA 138
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ENSVDSKSIK-NLEPKIIHGSESMDSGISLDNS-----YKMDYPEMGLCIIINNKNF
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        EDSVDAKPDRSSFVPSLFSKKKKNYTMRSIKTTRDRVPTYQYNMNFEKLGKCIIINNKNF 78
                                                                                                                                                                                                                                                                                                                                                                 SGPINDTDANPRYKIPVEADFLFAYSTVPGYYSWRSPGRGSWFVQALCSILEEHGKELEI 258
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  44.5%; Score 718; DB 5; 50.5%; Pred. No. 3.5e-73;
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US-08-964-313-10
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; MOLECULE TYPE:
US-08-964-308-10
                                                                                                                                                                                                                 Patent No.
                                                                                                                                                                                                                   Sequence 10, Application US/08964313 Patent No. 6114132
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Matches 143;
                                                                                                                                                                                              GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       INFORMATION FOR SEQ ID NO: SEQUENCE CHARACTERISTICS: LENGTH: 277 amino acid
                                                                                APPLICANT:
APPLICANT:
APPLICANT:
APPLICANT:
APPLICANT:
APPLICANT:
         TITLE OF INVENTION: PHOSPHATASE BINDING NUMBER OF SEQUENCES: 15
                                              APPLICANT:
APPLICANT:
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MEDIUM TYPE: Floppy Diskette
COMPUTER: IBM PC COMPATIBLE
OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 TELECOMMUNICATION INFORMATION:
TELEPHONE: 732-594-7262
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 SOFTWARE: FastSEQ for Windows Version CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ATTORNEY/AGENT INFORMATION:
NAME: NORTH, ROBERT J
                                                                                                                                                                                                                                                                                                                       233 MHILTRVNRKVATEFESFSFDATFHAKKQIPCIVSMLTKELYF
                                                                                                                                                                                                                                                                                                                                                259 MQILTRVNDRVARHFESQSDDPHFHEKKQIPCVVSMLTKELYF 301
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               139 CILLSHGEENVIYGKDGVTPIKDLTAHFRGDRCKTLLEKPKLFFIQACRGTELDDAIQAD 198
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OPERATING SYSTEM:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             19 EDSVDAKPDRSSFVPSLFSKKKKNVTMRSIKTTRDRVPTYQYNMNFEKLGKCIIINNKNF 78
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      REFERENCE/DOCKET NUMBER: 19
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              APPLICATION NUMBER: US/0:
FILING DATE: 04-NOV-1996
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    56 HKSTGMTSRSGTDVDAANLRETFRNLKYEVRNKNDLTREEIVELMRDVSKEDHSKRSSFV 115
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Local Similarity
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         TYPE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               CLASSIFICATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 COUNTRY:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ADDRESSEE: ROBERT J. NORTH - MERCK & CO., INC. STREET: 126 EAST LINCOLN AVENUE - P.O. BOX 2000
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         DKVTGMGVRNGTDKDAEALFKCFRSLGFDVIVYNDCSCAKMQDLLKKASEEDHTNAACFA 138
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ENSVDSKSIK-NLEPKIIHGSESMDSGISLDNS-----YKMDYPEMGLCIIINNKNF 55
                                                                                                                                                                                                                                                                                                                                                                                                  SGVDDDMAC---HKIPVEADFLYAYSTAPGYYSWRNSKDGSWFIQSLCAMLKQYADKLEF
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                                                                                                                                    FRIESEN, RICHARD
GRESSER, MICHAEL
                                          SKOREY, KATHRYN
FORD-HUTCHINSON, ANTHONY
                                                                                                   KENNEDY, BRIAN
NICHOLSON, DONALD
                                                                                RAMACHANDRAN, CHIDAMBARAN
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linear
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50.5%;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        19840 PCT
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78;

12;

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232

Length 277; Indels

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В õ 밁 ş 밁 οy 밁

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Search completed: December Job time: 16.1052 secs
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      INFORMATION FOR SEQ ID NO: 10
SEQUENCE CHARACTERISTICS:
LENGTH: 277 amino acids
TYPE: amino acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Query Match 44.1
Best Local Similarity 50.5
Matches 143; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 APPLICATE O3 -NOV-LOCAL PILING DATE: 03 -NOV-LOCAL PILING DATE: 03 -NOV-LOCAL PILING PRICE PROPERTY INFORMATION:

NAME: DURETTE, PHILIPPE L.

REGISTRATION NUMBER: 35,125

REFERENCE/DOCKET NUMBER: 19824Y

TELECOMMUNICATION INFORMATION:

TOT FEBRONE: 732-594-4568
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          OPERATING SYSTEM: DOS
OPERATING SYSTEM: DOS
SOFTWARE: FastSEQ for Windows Version 2.0
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/964,313
FILING DATE: 04-NOV-1997
CLASSIFICATION BATA:
CLASSIFICATION DATA:
APPLICATION NUMBER: 60/030,408
FILING DATE: 04-NOV-1996
APPLICATION NUMBER: PCT/CA97/00825
FILING DATE: 03-NOV-1996
APPLICATION NUMBER: PCT/CA97/00825
FILING DATE: 03-NOV-1996
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       COMPUTER READABLE FORM: MEDIUM TYPE: Diskette
                                                                        56 HKSTGMTSRSGTDVDAANLRETFRNLKYEVRNKNDLTREEIVELMRDVSKEDHSKRSSFV 115
                                                                                                                                                                                                                                                                                                                                                  79 DKYTGMGYRNGTDKDAEALFKCFRSLGFDYIYYNDCSCAKMQDLLKKASBEDHTNAACFA 138
                                                                                                                                                                                                                                                                                                                                                                                                                                      19 EDSVDAKPDRSSFVPSLFSKKKKNVTMRSIKTTRDRVPTYQYNMNFEKLGKCIIINNKNF 78
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         COMPUTER: IBM CONTROL OPERATING SYSTEM:
SOFTWARE: FastSE
                                                                                                                                                                                                                                                                                                                                                                                                            5 ENSVDSKSIK-NLEPKIIHGSESMDSGISLDNS-----YKMDYPEMGLCIIINNKNF 55
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                   2002, 12:58:44
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Post-processing: Minimum Match 0%
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Listing first 45 summaries
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2: /cgn2_6/ptodata/1/iaa/5B_COMB.pep:*
3: /cgn2_6/ptodata/1/iaa/6A_COMB.pep:*
4: /cgn2_6/ptodata/1/iaa/FB_COMB.pep:*
5: /cgn2_6/ptodata/1/iaa/PCTUS_COMB.pep:*
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US-09-969-138-6
US-09-969-1751-12
US-09-969-10521-30
PCT-US-96-964-313-10
US-08-964-313-10
US-08-964-313-10
US-08-964-313-11
US-09-561-756-24
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US-09-561-756-24
US-09-561-756-27
US-09-561-756-21
US-09-561-756-21
US-09-561-756-22
US-09-561-756-21
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; MOLECULE TYPE:
US-08-591-605-2
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US-08-591-605-2
                                                                                                                                                                                                                                                                                 APPLICATION NUMBER: US/08/591,605
FILING DATE: 09-FEB-1996
CLASSIFICATION: 514
ATTORNETYAGENT INFORMATION:
NAME: KONSKI, ANTOINETTE: F.
REGISTRATION NUMBER: 34,202
REFERENCE/DOCKET NUMBER: 20344-21036
TELECOMMUNICATION INFORMATION:
TELEPHONE: (415) 813-5600
TELEPHONE: (415) 813-5600
TELEPHONE: (415) 8494-0792
TELEX: 706141 MRSNFOERS SFO
INFORMATION FOR SEQ ID NO: 2:
SEQUENCE CHARACTERISTICS:
LENGTH: 277 amino acids
                                                                                                                                                  Best
                                                                                                                            Matches
                                                                                                                                                                     Query Match
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           GENERAL INFORMATION:
APPLICANT: Dixit, Vishva
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk.
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  CORRESPONDENCE ADDRESS:
ADDRESSEE: MORRISON & FOERSTER
STREET: 755 PAGE MILL ROAD
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               TITLE OF INVENTION:
TITLE OF INVENTION:
NUMBER OF SEQUENCES:
                                                                                                                          Local Similarity tes 277; Conserv
                                                                                                                                                                                                                                                                TYPE: amino acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            STREET: 755 PAGI
CITY: PALO ALTO
STATE: CA
61 MTSRSGTDVDAANLRETFRNLKYEVRNKNDLTREEIVELMRDVSKEDHSKRSSFVCVLLS 120
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   COUNTRY: USA
ZIP: 94304-1018
                                                              1 MENTENSVDSKSIKNLEPKIIHGSESMDSGISLDNSYKMDYPENGLCIIINNKNFHKSTG
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                                                                                                                                           100.0%; Score 1463; DB 3; 100.0%; Pred. No. 1.7e-161;
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METHOD AND COMPOSITION FOR REGULATING
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US-08-73-608A-2
US-08-773-608A-2
US-09-561-756-27
US-09-227-721-27
US-08-618-408B-4
US-08-983-502-18
PCT-US96-10521-7
PCT-US96-10521-7
US-08-983-502-7
PCT-US96-10521-7
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Patent No. 6066715
                                                                                                                                                                                                                                                                                               INFORMATION FOR SEQ ID NO: SEQUENCE CHARACTERISTICS:
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                                                                                                                                                                                                                           MOLECULE TYPE:
                                                                                                                                                                                                                                                                                                                                      TELECOMMUNICATION INFORMATION:
TELEPHONE: 732-594-7262
TELEFAX: 732-594-4720
                                                                                                                                                                                                                                                                                                                                                                                                                            ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           MEDIUM TYPE: Floppy
121 TGEEGIIFGTNGPVDLKKITNFFRGDRCRSLTGKPKLFIIQACRGTELDCGIETDSGVDD 180
                                                                                                                                                                                                               -964-308-6
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            NUMBER OF SEQUENCES: 1:
CORRESPONDENCE ADDRESS:
ADDRESSEE: ROBERT J.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         APPLICANT: FRIESEN, RICHARD
APPLICANT: ZAMBONI, ROBERT
TITLE OF INVENTION: NEW LIGANDS FOR PHOSPHATASE
TITLE OF INVENTION: BINDING ASSAY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  APPLICANT:
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                                                                                                                                                                                                                                          TOPOLOGY:
                                                                                                                                                                                                                                                                  TYPE: amino acid
                                                                                                                                                                                                                                                                                                                             TELEX:
                                                                                                                                                                                                                                                                                                                                                                                                                                       CLASSIFICATION: 530
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              COMPUTER: IBM PC Compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: FastSEQ for Windows Version
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REFERENCE/DOCKET NUMBER: 19
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                                                                                                  1 MENTENSVDSKSIKNLEPKIIHGSESMDSGISLDNSYKMDYPEMGLCIIINNKNFHKSTG 60
                                                                                                                                                                                                                                                                                                                                                                                              NAME: NORTH, ROBERT J
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         COUNTRY:
                                                                                                                                                                                                                                                                                   ENGTH:
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                                           MTSRSGTDVDAANLRETFRNLKYEVRNKNDLTREEIVELMRDVSKEDHSKRSSFVCVLLS 120
                            MTSRSGTDVDAANLRETFRNLKYEVRNKNDLTREEIVELMRDVSKEDHSKRSSFVCVLLS
                                                                                   MENTENSVDSKSIKNLEPKIIHGSESMDSGISLDNSYKMDYPEMGLCIIINNKNFHKSTG 60
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                                                                                                                                                                                                                                                                              277 amino acids
                                                                                                                                                    Conservative
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                                                                                                                                                             Score 1463; DB 3;
Pred. No. 1.7e-161;
                                                                                                                                                                                                                                                                                                                                                                                  19840 PCT
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US-08-462-969B-4
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TELEPHONE: 301-309-8504
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APPLICATION NUMBER: US 08/334,251
FILING DATE: 11-NOV-1994
                                                                                                                                                                                                                                                                                                                              SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             SOFTWARE: Patentin Rel
CURRENT APPLICATION DATA:
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         181
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CORRESPONDENCE ADDRESS:
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OTTY: Rockville
                                                                             Local Similarity
nes 277; Conserv
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                                                                                                                                                                                                                                                                                                                                                                                           NAME: Brookes, A. Anders
REGISTRATION NUMBER: 36,373
REFERENCE/DOCKET NUMBER: PF
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                                                                                                                                 STRANDEDNESS:
                                                                                                                                                                                                                                                                                                       TYPE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ZIP: 20850
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                         HGEEGIIFGTNGPVDLKKITNFFRGDRCRSLTGKPKLFIIQACRGTELDCGIETDSGVDD 180
DMACHKIPVEADFLYAYSTAPGYYSWRNSKDGSWFIQSLCAMLKQYADKLEFMHILTRVN 240
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Pred. No. 1.7e-161;
; Mismatches 0;
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Best Local 9
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                                                                                                                                                                                                                                                                                                              INFORMATION FOR SEQ ID NO:
                                                                                                                                                                                                                                                                                                                                                                                        FILING DATE: 03 - NOV-1996
ATTORNEY/AGENT INFORMATION:
NAME: DURETTE, PHILIPPE L.
REGISTRATION NUMBER: 35,125
REFERENCE/DOCKET NUMBER: 19824Y
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                                                                                                                                                                                                            TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: peptide
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MEDIUM TYPE: Diskette
                                                                                                                                                                                                                                                                           SEQUENCE CHARACTERISTICS:
LENGTH: 277 amino acids
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         SOFTWARE: FastSEQ for Windows Version CURRENT APPLICATION DATA:
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CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       APPLICANT: FORD-HUTCHINSON, ANTHONY
TITLE OF INVENTION: PHOSPHATASE BINDING ASSAY
                                                                                                                                                                                                                                                                                                                                                             TELECOMMUNICATION INFORMATION: TELEPHONE: 732-594-4568
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FILING DATE: 04-NOV-1996
APPLICATION NUMBER: PCT/CA97/00825
   61
                61 MTSRSGTDVDAANLRETFRNLKYEVRNKNDLTREEIVELMRDVSKEDHSKRSSFVCVLLS 120
                                                                                                                               Local Similarity les 277; Conserv
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             FILING DATE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          APPLICATION NUMBER: US/08/964,313
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                                                                             1 MENTENSVDSKSIKNLEPKIIHGSESMDSGISLDNSYKMDYPEMGLCIIINNKNFHKSTG
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MTSRSGTDVDAANLRETFRNLKYEVRNKNDLTREEIVELMRDVSKEDHSKRSSFVCVLLS
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SKOREY, KATHRYN
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6 EAST LINCOLN AVENUE - P.O. BOX 2000
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MICHAEL
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                                                                                                                              Score 1463; DB 3;
Pred. No. 1.7e-161;
Mismatches 0;
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                                                                                                                         Matches
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SEQUENCE CHARACTERISTICS:
LENGTH: 277 amino acids
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SOFTWARE: FastSEQ for Windows V
CURRENT APPLICATION DATA:
                                                                                                                                                                                                    MOLECULE TYPE:
                                                                                                                                                                                                                                                                                                                                                REFERENCE/DOCKET NUMBER: 19
TELECOMMUNICATION INFORMATION:
TELEPHONE: 732-594-4568
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APPLICANT: ZAMBONI, ROBERT
TITLE OF INVENTION: NEW LIGANDS FOR PHOSPHATASE
TITLE OF INVENTION: BINDING ASSAY
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              61 MTSRSGTDVDAANLRETFRNLKYEVRNKNDLTREEIVELMRDVSKEDHSKRSSFVCVLLS 120
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OPERATING SYSTEM:
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TELEFAX: 732-594-4720
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         MEDIUM TYPE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     STREET: 126 | CITY: RAHWAY
                                                                                                                                        Local Similarity
                                                                                                                                                                                                                                  STRANDEDNESS: single
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                                                                           1 MENTENSVDSKSIKNLEPKIIHGSESMDSGISLDNSYKMDYPEMGLCIIINNKNFHKSTG
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MTSRSGTDVDAANLRETFRNLKYEVRNKNDLTREEIVELMRDVSKEDHSKRSSFVCVLLS
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         USA
                                                                                                                       100.0%; Silarity 100.0%; FConservative 0;
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FRIESEN, RICHARD
LEBLANC, YVES
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Pred. No. 1.7e-161;
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RESULT 7
US-09-227-721-12
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US-09-561-756-12
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CURRENT APPLICATION NUMBER: US/09/227,721
CURRENT FILING DATE: 1999-01-08
NUMBER OF SEQ ID NOS: 116
SOFTWARE: FastSEQ for Windows Version 3.0
SEQ ID NO 12
                                                                                                                                                                                                                                                                        Sequence 12, Application US/09227721 Patent No. 6379950 GENERAL INFORMATION:
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PRIOR FILING DATE: 1999-01-08
NUMBER OF SEQ ID NOS: 116
SOFTWARE: FastSEQ for Windows Version
SEQ ID NO 12
LENGTH: 277
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                                                                                                                                                   APPLICANT: Alnemri, Emad S.
TITLE OF INVENTION: RECOMBINANT, ACTIVE CASPASES AND USES
TITLE OF INVENTION: THEREOF
FILE REFERENCE: 480140.431
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         GENERAL INFORMATION:
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TITLE OF INVENTION: RECOMBINANT, ACTIVE CI
TITLE OF INVENTION: THEREOF
FILE REFERENCE: 480140, 431
CURRENT APPLICATION NUMBER: US/09/561,756
CURRENT FILING DATE: 2000-04-26
DELICO NOTICE STATEMENT OF THE STATEMENT OF
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ORGANISM: Homo sapien
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Pred. No. 3.7e-161;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Query Match
Best Local Similarity
Matches 276; Conserv
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TYPE: PRT
PRIOR APPLICATION NUMBER: IL 11
APPLICATION NUMBER: IL 11
APPLICATION NUMBER: IL 11
TORRES 17-DEC-1995
                                                                                                                                                                                                                                    CURRENT APPLICATION DATA:
APPLICATION NUMBER: US,
FILING DATE: 16-JAN-19
                                                                                                                                                                                                                                                                                                                                                                                                                                                                      APPLICANT: DAVID WALLACH
APPLICANT: MAYE P. BOLDIN
APPLICANT: Tanya M. GONCHAROV
APPLICANT: YUTY V. GOLTSEV
TITLE OF INVENTION: MODULATORS OF THE FUNCTION OF FAS RECEPTORS
TITLE OF INVENTION: AND OTHER PROTEINS
                                                                                                                                                                                                                 PRIOR APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                       COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
                                                                                  PRIOR APPLICATION DATA:
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CITY: Washington
STATE: D.C.
COUNTRY: USA
ZIP: 20004
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       APPLICATION NUMBER: FILING DATE: 14-JUN
                                                                                                                                                                                                                                                                    COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
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                                                                                                 FILING DATE: 17-AUG-1995
                                                                                                                                          FILING DATE:
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                                                                                                              APPLICATION NUMBER:
                                                                                                                                                           APPLICATION NUMBER:
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No. 6399327
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                                                                                                                                                                                       NUMBER: PCT/US96/10521
14-JUN-1996
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                                                                                                               IL 114,986
                                                                                                                                                         IL 114,615
                                                                    IL 115,319
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Pred. No. 3.7e-161;
1; Mismatches 0;
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PCT-US96-10521-30
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Best Local Similarity
Matches 276; Conserv
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INFORMATION FOR SEQ ID NO:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                              PRIOR APPLICATION DATA:
APPLICATION NUMBER: IL 1:
FILING DATE: 16-JUL-1995
                                                                                                                                                                                                                                                                 CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                             COMPUTER READABLE FORM:
                                                                                                                                                                                                                                                                                                                                                            TITLE OF INVENTION:
TITLE OF INVENTION:
NUMBER OF SEQUENCES:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       TELEPHONE: (202) 628-5197
                                                PRIOR APPLICATION DATA:
                                                                                              FILING DATE: 17-AUG-
                                                                                                                                                                                                                                                                                                                                                                                                                APPLICANT:
                                                                                                                                                PRIOR APPLICATION DATA:
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                  APPLICATION NUMBER: FILING DATE: 27-DEG
                                                                   APPLICATION NUMBER: FILING DATE: 14-SEP
                                                                                                             APPLICATION NUMBER: IL 1. PILLING DATE: 17-AUG-1995
                                                                                                                                                                                                               CLASSIFICATION:
                                                                                                                                                                                                                                                                           SOFTWARE: PatentIn Release #1.0, Version #1.30 (EPO)
                                                                                                                                                                                                                                                                                              COMPUTER: IBM PC compatible OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                                MEDIUM TYPE: Floppy disk COMPUTER: IBM PC compati
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STRANDEDNESS: sir
TOPOLOGY: linear
                                                                                                                                                                                                                                   FILING DATE
                                                                                                                                                                                                                                                APPLICATION NUMBER:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    61 MTSRSGTDVDAANLRETFRNLKYEVRNKNDLTREEIVELMRDVSKEDHSKRSSFVCVLLS 120
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     MENTENSVDSKSIKNLEPKIIHGSESMDSGISLDNSYKMDYPEMGLCIIINNKNFHKSTG 60
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     APPLICATION
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                                                                 TUMBER: IL 115,319
14-SEP-1995
                  27-DEC-1995
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        99.8%; Score 1460; DB 4; 99.6%; Pred. No. 3.7e-161;
                                 IL 116,588
                                                                                                                                                                                IL 114,615
                                                                                                                              IL 114,986
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    Mismatches

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               INFORMATION FOR SEQ ID NO:
SEQUENCE CHARACTERISTICS:
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RESULT 10
US-08-964-308-10
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                                                                                                                                                                                                                                                                                                                                                                         CIP: U/VU-
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy Diskette
COMPUTER: IBM PC Compatible
COMPUTER: IBM PC COMPATIBLE SYSTEM: PC-DOS/MS-DOS
SOFTWARE: FSSESSO for Windows Version 2.
CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Patent No.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Sequence 10,
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Matches 276; Conserva
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                                                                       CLASSIFICATION: 530
ATTOREY/AGENT INFORMATION:
NAME: NORTH, ROBERT J
REGISTRATION NUMBER: 27,366
REFERENCE/DOCKET NUMBER: 198
TELECOMMUNICATION INFORMATION:
TELEDHONE: 732-594-7262
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  GENERAL INFORMATION:
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ADDRESSEE: ROBERT J. NORTH - MERCK & CO.,
STREET: 126 EAST LINCOLN AVENUE - P.O. BO
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                APPLICANT: FRIESEN, RICHARD
APPLICANT: ZAMBONI, ROBERT
TITLE OF INVENTION: NEW LIGANDS FOR PHOSPHATASE
TITLE OF INVENTION: BINDING ASSAY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    APPLICANT:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              NUMBER OF SEQUENCES:
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TELEPHONE: /32 - TELEPH
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    241 RKVATEFESFSFDATFHAKKQIPCIVSMLTKELYFYH 277
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             STATE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      61 MTSRSGTDVDAANLRETFRNLKYEVRNKNDLTREEIVELMRDVSKEDHSKRSSFVCVLLS 120
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STRANDEDNESS: sir
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Pred. No. 3.7e-161;
                                                                                                                                                           19840 PCT
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; STRANDEDNESS:
; TOPOLOGY: line
; MOLECULE TYPE: F
US-08-964-308-10
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US-08-964-313-10
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  APPLICANT:
APPLICANT:
                                     FILING DATE: 04-NOV-1996
APPLICATION NUMBER: PCT/CA97/00825
FILING DATE: 03 -NOV-1996
ATTORNEY/AGENT INFORMATION:
NAME: DURESTE, PHILIPPE L.
                                                                                                                                                                      SOFTWARE: FASTEM: DOS
SOFTWARE: FASTEE for Windows Version
CURRENT APPLICATION DATA:
APPLICATION NUMBER
                                                                                                                                                                                                                                                                                                                                                                                                                                                         APPLICANT:
                                                                                                                                                                                                                                                  COMPUTER READABLE FORM: MEDIUM TYPE: Diskette
TELECOMMUNICATION INFORMATION:
                                                                                                                               PRIOR APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                    CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                    NUMBER OF SEQUENCES:
                                                                                                                                                                                                                                                                                                                                                                                                 TITLE OF INVENTION:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       121
            NAME: DURETTE, PHILIPPE L. REGISTRATION NUMBER: 35,125 REFERENCE/DOCKET NUMBER: 19
                                                                                                                                                                                                                                                                                            COUNTRY:
                                                                                                                                                                                                                                   COMPUTER:
                                                                                                                                                                                                                                                                                                                                       STREET:
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                                                                                                                APPLICATION NUMBER: 60/030,408
                                                                                                                                              CLASSIFICATION:
                                                                                                                                                             FILING DATE:
                                                                                                                                                                                                                                                                                                                                                        ADDRESSEE:
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                                                                                                                                                                                                                                                                                            USA
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GRESSER, MICHAEL
KENNEDY, BRIAN
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                                                                                                                                                                                                                                                                                                                                                                                                                                         RAMACHANDRAN, CHIDAMBARAN
                                                                                                                                                                                                                                                                                                                                                                                                                                                          NICHOLSON, DONALD
                                                                                                                                                                                                                                                                                                                                                                                                                               SKOREY, KATHRYN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 DESMARAIS,
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                                                                                                                                                                                                                                IBM Compatible
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Pred. No. 2
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Patent No.
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Best Local Similarity
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                                                                                                                   COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy Diskette
COMPUTER: IBM PC COMPATIBLE
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: FastesQ for Windows Version
CURRENT APPLICATION DATA:
                          CLASSIFICATION: 530
ATTORNEY/AGENT INFORMATION:
NAME: DURETTE, PHILIPPE L.
REGISTRATION NUMBER: 35,12
                                                                                                                                                                                                                                                                                                               APPLICANT: YOUNG, ROBERT N.
APPLICANT: ZAMBONI, ROBERT
TITLE OF INVENTION: NEW LIGANDS FOR PHOSPHATASE
TITLE OF INVENTION: BINDING ASSAY
NUMBER OF SEQUENCES: 15
TELECOMMUNICATION INFORMATION:
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ZIP: 07065
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                                                                                       APPLICATION NUMBER: US/09/069,138 FILING DATE: 29-APR-1998
                                                                                                                                                                                                                                                       STREET: 126
CITY: RAHWAY
               REFERENCE/DOCKET NUMBER:
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TYPE: amino acid
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FRIESEN, RICHARD
LEBLANC, YVES
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99.6%;
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LN AVENUE - P.O. BOX 2000
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Pred. No. 2.4e-160;
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Best Local Similarity
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INFORMATION FOR SEQUENCE CHARA
                                                                                                                                                                                                                                                                                                                                                                                                                                  tent No.
                                                                                                                                                                                                                                                                                                                                TITLE OF INVENTION:
TITLE OF INVENTION:
NUMBER OF SEQUENCES:
                                      REFERENCE/DOCKET NUMBER: X-
TELECOMMUNICATION INFORMATION:
TELEPHONE: (317) 276-0756
                                                                          CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: Gaylo, Paul J.
REGISTRATION NUMBER: 36,808
                                                                                                                                                                                                                                                                                                                      CORRESPONDENCE ADDRESS:
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                                                                                                                                                           CURRENT APPLICATION DATA:
                                                                                                                                                                                                                            COMPUTER READABLE FORM:
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TELEX:
                                                                                                                                                                                                                                                                  STREET: Lilly Corp. CITY: Indianapolis STATE: Indiana
                                                                                                                    APPLICATION NUMBER: US/08/890,542A FILING DATE: 09-JUL-1997 CLASSIFICATION: 435
                                                                                                                                                                      MEDIUM TYPE: Floppy disk
COMPUTER: IEM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     TYPE: amino acid
STRANDEDNESS: sin
TOPOLOGY: linear
                                                                                                                                                                                                                                                   COUNTRY:
                            TELEFAX:
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5840509
    CHARACTERISTICS:
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             (317) 276-3861
OR SEQ ID NO: 2:
                                                                                                                                                                                                                                                    United States
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linear
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Pred. No. 2.
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US-09-561-756-34
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                                                                                                                                                                              Query Match
Best Local Similarity
Matches 175; Conserv
                                                                                                                                                                                                                                                                                                                                              SOFTWARE: FastSEQ for Windows Version SEQ ID NO 34
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Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                          APPLICANT: Alnemai, Emad S.
APPLICANT: Alnemai, Emad S.
TITLE OF INVENTION: RECOMBINANT, ACTIVE CASPASES
TITLE OF INVENTION: THEREOF
FILE REFERENCE: 480140.431
CURRENT APPLICATION NUMBER: US/09/561,756
CURRENT FILING DATE: 2000-04-26
PRIOR APPLICATION NUMBER: 09/227,721
PRIOR FILING DATE: 1999-01-08
NUMBER OF SEQ ID NOS: 116
                                                                                                                                                                                                                                                                                             LENGTH: 290
TYPE: PRT
ORGANISM: Artificial Sequence
                                                                                                                                                                                                                                                                                  FEATURE:
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Pred. No. 4.9e-143;
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RESULT 15 US-09-227-721-34

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Requence 34, Application US/09227721

Patent No. 637950

GENERAL INFORMATION:
APPLICANT: Alnemri, Emad S.
TITLE OF INVENTION: RECOMBINANT, ACTIVE CASPASES AND USES
TITLE OF INVENTION: THEREOF
FILE REFERENCE: 480140, 431

CURRENT PILING DATE: 1999-01-08

NUMBER OF SED ID NOS: 116

SOFTWARR: FASTSEQ for Windows Version 3.0

LENGTH: 290
TYPE: PRT
ORGANISM: Artificial Sequence
FEATURE:
OTHER INFORMATION: Rev-Caspase-3 constructed from human caspase -3

US-09-227-721-34

OUS-09-227-721-34

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Minimum DB
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US-09-895-263-4
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9, A	31	4795	27,	15,	14,	34,		24,	4	5	2	Sequence 2, Appli	9	2, 1	e 24,	36	4	21	e 2,	ው	e 28,	e 2, Appl	e 2	e 33,	Sequence 2, Appli

ALIGNMENTS

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Sequence 4, Application US/09895263
Patent No. US20020076793A1
GENERAL INFORMATION:
APPLICANT: He, Wei-Wu et al.
TITLE OF INVENTION: Interleukin-1 Beta Converting Enzyme
Like Apoptosis Protease 3 and 4
                                                                                                           REFERENCE/DOCKET NUMBER: I
TELECOMMUNICATION: INFORMATION:
TELEPHONE: 301-251-6015
TELEFAX: 301-309-8439
INFORMATION FOR SEQ ID NO: 4:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                    APPLICATION NUMBER: <Unknown>
FILING DATE: <Unknown>
ATTORNEY/AGENT INFORMATION:
NAME: Jonathan L. Klein
REGISTRATION NUMBER: 41,119
                                                                                                                                                                                                                                                                                                                                                                                                                                                             ZIP: 20850

COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                       APPLICATION NUMBER: US/09/895,263
FILING DATE: 02-Jul-2001
CLASSIFICATION: -Unknown>
PRIOR APPLICATION DATA:
MOLECULE TYPE: protein
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ADDRESSEE: Human G
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                                           STRANDEDNESS: single
                                                                     TYPE: amino acid
                                                                                           LENGTH: 277 amino acids
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                          TOPOLOGY:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        STATE: MD
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US-09-954-697-12
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US-09-895-263-4
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PATENT NO. US2002016631A1
GEMERAL INFORMATION:
APPLICANT: Alnemri, Emad S.
TITLE OF INVENTION: RECOMBINANT, ACTIVE CASPASES
TITLE OF INVENTION: THEREOF
FILE REFERENCE: 480140.431D2
                                                                                                                                                                                                                                  Best Local Si
Matches 276;
                                                                                                                                                                                                                                                                                                     CURRENT APPLICATION NUMBER: US/09/954,697
CURRENT FILING DATE: 2001-09-14
NUMBER OF SEQ ID NOS: 116
SOFTWARE: FastSEQ for Windows Version 3.0
SEQ ID NO 12
LENGTH: 277
TYPE: PRT
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Best Local
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         RKVATEFESFSFDATFHAKKQIPCIVSMLTKELYFYH 277
                                         DMACHKIPVDADFLYAYSTAPGYYSWRNSKDGSWFIQSLCAMLKQYADKLEFMHILTRVN
                                                    DMACHKIPVEADFLYAYSTAPGYYSWRNSKDGSWFIQSLCAMLKQYADKLEFMHILTRVN
                                                                                                   HGEEGIIFGTNGPVDLKKITNFFRGDRCRSLTGKPKLFIIQACRGTELDCGIETDSGVDD
                                                                                                                                    MTSRSGTDVDAANLRETFRNLKYEVRNKNDLTREEIVELMRDVSKEDHSKRSSFVCVLLS
                                                                                                                                                MTSRSGTDVDAANLRETFRNLKYEVRNKNDLTREEIVELMRDVSKEDHSKRSSFVCVLLS 120
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                                                                                       HGEEGIIFGTNGPVDLKKITNFFRGDRCRSLTGKPKLFIIQACRGTELDCGIETDSGVDD
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Pred. No. 2.1e-136;
1; Mismatches 0;
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Pred. No. 1.1e-136;
; Mismatches 0;
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RESULT 3

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; LENGTH: 264
; TYPE: PRT
; ORGANISM: HOMO s
US-10-103-448-3
                                                               ; OTHER INFORMATION: Rev-Caspase-3 contructed from human caspase US-09-954-697-34
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                                                                                                                                        TITLE OF INVENTION: RECOMBINANT, ACTIVE CASPASES TITLE OF INVENTION: THEREOF FILE REFERENCE: 480140.431D2 CURRENT APPLICATION NUMBER: US/09/954,697 CURRENT FILING DATE: 2001-09-14 NUMBER OF SEQ ID NOS: 116 SOFTWARE: FastSEQ for Windows Version 3.0 SEQ ID NO 34
      Matches
                   Query Match
Best Local S
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Best Local Similarity
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APPLICANT: Fritz, Lawrence C.
APPLICANT: Wu, Joseph C.
APPLICANT: Wu, Joseph C.
TITLE OF INVENTION: MEMBRANE DERIVED CASPASE-3,
TITLE OF INVENTION: COMPRISING THE SAME AND MET
                                                                                          LENGTH: 290
TYPE: PRT
ORGANISM: Artificial Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           FILE REFERENCE: 480140.468D1
CURRENT APPLICATION NUMBER: US/10/103,448
CURRENT FILING DATE: 2002-03-20
NUMBER OF SEQ ID NOS: 7
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                   Similarity
   62.3%;
ilarity 100.0%;
Conservative
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 Score 912; DB 10;
; Pred. No. 2.2e-82;
0; Mismatches 0;
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Pred. No. 3.1e-130;
1; Mismatches 0;
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THODS OF USE
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                              Length 290
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RESULT 6
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                                   ; LENGTH: 182
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-809-905-2
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     Query Match
                                                                                                     SOFTWARE: PatentIn Ver. 2.1
SEQ ID NO 2
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Best Local
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                                                                                                                                                                                     APPLICANT: Huang, Yuanhui
APPLICANT: Sun, Yi
APPLICANT: Wang, Kevin Ka-Wang
TITLE OF INVENTION: CASPASE-3S SPLICING VI
FILE REFERENCE: U.S. Application A0000224
CURRENT APPLICATION NUMBER: US/09/809,905
CURRENT FILING DATE: 2001-03-16
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                                                                                                                                       PRIOR APPLICATION NUMBER: 60/204,468 PRIOR FILING DATE: 2000-05-16 NUMBER OF SEQ ID NOS: 5
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CURRENT FILING DATE: 2001-09-14
NUMBER OF SEQ ID NOS: 116
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TYPE: PRT
ORGANISM: Artificial Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  FEATURE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                       121
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98.9%;
   56.9%;
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 Score 833;
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Pred. No. 7.9e-81;
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 DB 10;
Length 182;
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Дb
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                                                                                      Matches 145;
                                                                                                     Query Match
Best Local Similarity
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                                                                                                                                                                                                                                                                                                                   INFORMATION FOR SEQ ID NO:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   121 HGEEGIIFGTNGPVDLKKITNFFRGDRCRSLTGKPKLFIIQ 161
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                                      5 ENSVDSKSIK-NLEPKIIHGSESMDSGISLDNS-----YKMDYPEMGLCIIINNKNF
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                                                                                                                                                                                                                                                                                                                                                                                                                APPLICATION NUMBER: 08/556,627
FILING DATE: 13-NOV-1995
ATTORNEY/AGENT INFORMATION:
NAME: Campbell, Cathryn A.
REGISTRATION NUMBER: 31,815
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         APPLICATION NUMBER: US/09/944,851
FILING DATE: 31-Aug-2001
CLASSIFICATION: -Unknown>
PRIOR APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                              SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                             TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                COMPUTER READABLE FORM:
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ADDRESSEE: Campbell and Flores
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     TITLE OF INVENTION: Mch3, A No. US20020102648A1el Apoptotic Protease, Nucleic Acids Encoding and Methods of Use
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      NUMBER OF SEQUENCES: 11
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    APPLICANT: Alnemri, Emad S
EDSVDAKPDRSSFVPSLFSKKKKNVTMRSIKTTRDRVPTYQYNMNFEKLGKCIIINNKNF 78
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                                                                                                                                                                                                                                                   LENGTH: 303 amino acids TYPE: amino acid
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TELEFAX: (619) 535-8949
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        COMPUTER: IBM PC COMPATIBLE
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
                                                                                                                                                                                                                                                                                                                                                                                                   REFERENCE/DOCKET NUMBER: P-ID 1813
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                                                                                      Conservative
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Tomaselli, Kevin
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Litwack, Gerald
                                                                                                     49.6%; Score 725; DB 10; 51.2%; Pred. No. 6.1e-64;
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                                                                                 Mismatches
                                                                                                                          DB 10;
                                                                                                                      Length 303;
                                                                                 Indels
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RESULT 9
US-09-895-263-2
; Sequence 2, Application US/09895263
; Patent No. US20020076793A1
; GENERAL INFORMATION:
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US-09-954-697-24
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LENGTH: 303
TYPE: PRT
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Best Local Similarity
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     CURRENT APPLICATION NUMBER: US/09/954,697 CURRENT FILING DATE: 2001-09-14
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             NUMBER OF SEQ ID NOS: 116
SOFTWARE: FastSEQ for Windows Version 3.0
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          NUMBER OF SEQUENCES: 12
CORRESPONDENCE ADDRESS:
ADDRESSEE: Human Genome Sciences,
STREET: 9410 Key West Ave.
                                                                                AL INFURMATION.
APPLICANT: He, Wei-Wu et al.
TITLE OF INVENTION: Interleukin-1 Beta Converting
Tike Apoptosis Protease 3 and
                                                                                                                                                                                                                                                                                    MHILTRVNRKVATEFESFSFDATFHAKKQIPCIVSMLTKELYF 275
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CITY: Rockville
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US-09-954-697-21
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                                                                              GENERAL INFORMATION:
APPLICANT: Alhemri, Emad S.
TITLE OF INVENTION: RECOMBINANT, ACTIVE CASPASES
TITLE OF INVENTION: THEREOF
FILE REFERENCE: 480140.431D2
CURRENT APPLICATION NUMBER: US/09/954,697
CURRENT FILING DATE: 2001-09-14
      NUMBER OF SEQ ID NOS:
SOFTWARE: FastSEQ for
SEQ ID NO 21
LENGTH: 293
                                                                                                                                                                                                                       Sequence 21, Application US/09954697 Patent No. US20020106631A1
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TELEFAX: 301-309-8439
INFORMATION FOR SEQ ID NO: 2:
                                                                                                                                                                                                                                                                                                                                               259
                                                                                                                                                                                                                                                                                                                                                                                                                                     176 SGVDDDMAC----KKIPVEADFLYAYSTAPGYYSWRNSKDGSWFIQSLCAMLKQYADKLEF
                                                                                                                                                                                                                                                                                                                                                             233 MHILTRVNRKVATEFESFSFDATFHAKKQIPCIVSMLTKELYF 275
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MOLECULE TYPE: protein
SEQUENCE DESCRIPTION: SEQ ID
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              REFERENCE/DOCKET NUMBER: TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         APPLICATION NUMBER: <Unknown>
FILING DATE: <Unknown>
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              SOFTWARE: PatentIn Release #1.0, CURRENT APPLICATION DATA:
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MEDIUM TYPE: Floppy disk
                                                                                                                                                                                                                                                                                                                                        MQILTRVNDRVARHFESQSDDPHFHEKKQIPCVVSMLTKELYF
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FILING DATE: 02-Jul-2001
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   COMPUTER: IBM PC compatible OPERATING SYSTEM: PC-DOS/MS-DOS
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      COUNTRY:
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                                            Windows Version
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Pred. No. 1.5e-63;
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Length 303; Indels

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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  CURRENT APPLICATION NUMBER: US/09/954,697
CURRENT FILING DATE: 2001-09-14
NUMBER OF SEQ ID NOS: 116
SOFTWARE: FastSEQ for Windows Version 3.0
SEQ ID NO 27
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Sequence 27, Application US/09954697 Patent No. US20020106631A1 GENERAL INFORMATION:
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Best Local Similarity 41.5
Matches 105; Conservative
                                                                                                                                                                                                                                                                                                                                                                                Matches 103;
                                                                                                                                                                                                                                                                                                                                                                                                                      Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        APPLICANT: Alnemri, Emad S.
TITLE OF INVENTION: RECOMBINANT, ACTIVE CASPASES AND USSES
TITLE OF INVENTION: THEREOF
FILE REFERENCE: 480140.431D2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              LENGTH: 476
TYPE: PRT
445 YEVSNK-----DDKKNMGKQMPQPTFTLRKKLVF 473
                                           241
                                                                              385
                                                                                                                                                                                                                                                                                                          205
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                                                                                                                                                                                                                         265 GALTTTFEELHFEIKPHHDCTVEQIYEILKIYQLMDHSNMDCFICCILSHGDKGIIYGTD 324
                                                                                                                                                                                                                                                                                                                                                                                                  Local Similarity
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               264 CIVSMLTKELYFY 276
                                                                                                                                                                                                                                                                                                                                         19 KIIHGSESMDSGISLDNSYKMDYPEMGLCIIINNKNFHKST-----GMTSRSGTDVDA 71
                                                                                                                                                                                                                                                               72 ANLRETFRNLKYEVRNKNDLTREEIVELMRDVSKEDHSKRSSFVCVLLSHGEEGIIFGTN 131
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      97 LLKIHEVSTVSHADADCFVCVFLSHGEGNHIYAYDAKIEIQTLTGLFKGDKCHSLVGKPK 156
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   37 YKMDYPEMGLCIIINNKNFHKSTGMTSRSGTDVDAANLRETFRNLKYEVRNKNDLTREEI 96
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        37
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    RKVATEFESFSFDATFHAKKQIPCIVSMLTKELYF 275
                                                                                                                                                                    G-PVDLKKITNFFRGDRCRSLTGKPKLFIIQACRGTELDCGI--ETDSG----VDDDMAC 184
                                                                      POTRYIPDEADFLIGMATVNNCVSYRNPAEGTWYIQSLCQSLRERCPRGDDILTILTEVN
                                                                                                           HK----IPVEADFLYAYSTAPGYYSWRNSKDGSWFIQSLCAMLKQYADK-LEFMHILTRVN 240
                                                                                                                                                 GQEAPIYELTSQFTGLKCPSLAGKPKVFFIQACQGDNYQKGIPVETDSEEQPYLEMDLSS
                                                                                                                                                                                                                                                                                                    KIINDYEEFSKGEELCKVYQMKSKPRGYCLIINNHNFAKAREKVPKLHSIRDRNGTHLDA 264
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               YSHRETVNGSWYIQDLCEMLGKYGSSLEFTELLTLVNRKVSQRRVDFCKDPSAIGKKQVP
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             IFIIQACRGNQHDVPVIPLDVVDNQTEKLDTNITEVDAASVYTLPAGADFLMCYSVAEGY
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                                                                                                                                                                                                                                                                                                                                                                                Conservative
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41.5%; Pred. No. 2.6e-44;
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                                                                                                                                                                                                                                                                                                                                                                            Score 429; DB 10;
Pred. No. 1.7e-34;
9; Mismatches 99;
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                                                                                                                                                                                                                                                                                                                                                                                                                  Length 476;
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RESULT 12

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APPLICANT: Heinrikson, Robert I.
APPLICANT: Tomasselli, Alfredo G.
TITLE OF INVENTION: Method for Autoactivation of Procaspase 8
FILE REFERENCE: Docket No. US20020045205A1 6172
CURRENT APPLICATION NUMBER: US/09/862,915
CURRENT FILING DATE: 2001-05-22
NUMBER OF SEQ ID NOS: 4
SOFTWARE: Patentin Ver. 2.0
SEQ ID NO 1
LENGTH: 286
TYPE: PRT
ORGANISM: Homo sapiens
US-09-862-915-1
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SEQ ID NO 20
LENGTH: 479
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Best Local Similarity
                                                                        NUMBER OF SEQ ID NOS: 27
SOFTWARE: FastSEQ for Wi
                                                                                                                                                PRIOR APPLICATION NUMBER: PCT/EP98/01857
PRIOR FILING DATE: 1998-03-31
PRIOR APPLICATION NUMBER: GERMANY 197 13 393.2
PRIOR FILING DATE: 1997-04-01
                                                                                                                                                                                                                                                                                                     APPLICANT: French, E. Lars
TITLE OF INVENTION: FLIP GENES AND FLIP PROTEINS
FILE REFERENCE: 11141-002001
CURRENT APPLICATION NUMBER: US/09/410,194
CURRENT FILING DATE: 1999-09-30
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APPLICANT:
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APPLICANT: Thome, N
APPLICANT: Burns, F
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Rimoldi, Donata
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Bodmer, Jean-Luc
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; Pred. No: 3.2e-34;
49; Mismatches 96;
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; ORGANISM: Homo sapiens US-09-410-194-20

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; MOLECULE TYPE: protein ; SEQUENCE DESCRIPTION: SEQ ID NO: US-09-952-768-4
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Query Match
Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Matches 102;
                                                                                                                         TELEFAX: (206) 682-6031 INFORMATION FOR SEQ ID NO: 4:
                                                                                                                                                                                                                                                                                COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Ve:
CURRENT APPLICATION NUMBER: US/09/952,768
FILING DATE: 10-Sep-2001
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               136 LKKITNFFRGDRCRSLTGKPKLFIIQACRGTELDCGI--ETDSG-----VDDDMACHK----
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         33 IYELTSQFTGLKCPSLAGKPKVFFIQACQGDNYQKGIPVETDSEEQPYLEMDLSSPQTRY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           273
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       217 SESQ----TLDKVYQMKSKPRGYCLIINNHNFAKAREKVPKLHSIRDRNGTHLDAGALTT 272
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             77
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        24 SESMDSGISLDNSYKMDYPEMGLCIIINNKNFHKST-----GMTSRSGTDVDAANLRE 76
                                                                                                                                                                                                           CLASSIFICATION: <Unknown>
ATTORNEY/AGENT INFORMATION:
NAME: Christiansen, William T.
REGISTRATION NUMBER: 44,614
                                                                                     SEQUENCE CHARACTERISTICS:
LENGTH: 496 amino acids
                                                                                                                                                                           REFERENCE/DOCKET NUMBER: 480140.424C4 TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              NUMBER OF SEQUENCES:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           APPLICANT:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  EFESFSFDATFHAKKQIPCIVSMLTKELYF 275
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    IPVEADFLYAYSTAPGYYSWRNSKDGSWFIQSLCAMLKQYADK-LEFMHILTRVNRKVAT 245
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                TFEELHFEIKPHDDCTVEQIYEILKIYQLMDHSNMDCFICCILSHGDKGIIYGTDGQEAP 332
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 TFRNLKYEVRNKNDLTREEIVELMRDVSKEDHSKRSSFVCVLLSHGEEGIIFGTNG-PVD 135
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      IPDEADFLLGMATVNNCVSYRNPAEGTWYIQSLCQSLRERCPRGDDILTILTEVNYEVSN 452
                                                TOPOLOGY: linear
                                                                      TYPE: amino acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                STATE: Washington COUNTRY: USA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     CITY: Seattle
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ADDRESSEE: Seed Intellectual Property Law Group STREET: Suite 6300, 701 Fifth Avenue
                                                                                                                                                            TELEPHONE: (206) 622-4900
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   QF
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         INVENTION: MCH4 AND MCH5, NUCLEIC ACIDS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Alnemri, Emad S.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Tomaselli, Kevin
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Armstrong, Robert
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Litwack, Gerald
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Fernandes-Alnemri,
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Pred. No. 1e-33;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         AND METHODS
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      GENERAL INFORMATION:
APPLICANT: Srinivasula, Srinivasa M.
APPLICANT: Fernandes-Alnemii, Teresa
APPLICANT: Fernandes-Alnemii, Teresa
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            SOFTWARE: FastSEQ for SEQ ID NO 1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Sequence 1, Application US/10068569 Patent No. US20020160975A1
                                                                                                                                                                                                                                                                                                                                                       Matches
                                                                                                                                                                                                                                                                                                                                                                       Best
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Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              CURRENT APPLICATION NUMBER: US/10/068,569
CURRENT FILING DATE: 2002-02-06
NUMBER OF SEQ ID NOS: 28
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               TITLE OF INVENTION: A CONSERVED XIAP-INTERACTION MOTIF IN TITLE OF INVENTION: CASPASE-9 AND SMAC/DIABLO FOR MEDIATING APOPTOSIS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     FILE REFERENCE: 480140.475
                                                                                                                                                                                                                                                                                                                                                                                                                                     LENGTH: 416
TYPE: PRT
ORGANISM: Homo sapiens
   390
                                      242
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                                                                                                                                                                                                                                                                            150 DLAYILSMEPCGHCLIINNVNFCRESGLRTRTGSNIDCEKLRRRFSSLHFMVEVKGDLTA 209
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             136
                                                                                                                                                                        146 DRCRSLTGKPKLFIIQACRGTELDCGIETDSGVDDDM-----
                                                                                                                                                                                                           210 KKMVLALLELAQQDHGALDCCVVVILSHGCQASHLQFPGAVYGTDGCPVSVEKIVNIFNG
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                                                                                                                                                                                                                                                 94
                                                                                                                                                                                                                                                                                                               34 DNSYKMDYPEMGLCIIINNKNFHKSTGMTSRSGTDVDAANLRETFRNLKYEVRNKNDLTR 93
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   246 EFESFSEDATFHAKKQIPCIVSMLTKELYF 275
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   AVSVK - - .
                                KVATEFESFSFDATFHAKKQIPCIVSMLTKELYF 275
                                                                   DAISSLPTPSDIFVSYSTFPGFVSWRDPKSGSWYVETLDDIFEQWAHSEDLQSLLLRVAN
                                                                                                                                    {\tt TSCPSLGGKPKLFFIQACGGEQKDHGFEVASTSPEDES} {\tt PGSNPEPDATPFQEGLRTFDQL}
                                                                                                                                                                                                                                            EEIVELMRDVSKEDHSKRSSFVCVLLSHGEE-----GIIFGTNG-PVDLKKITNFFRG 145
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           LKKITNFFRGDRCRSLTGKPKLFIIQACRGTELDCGI--ETDSG----VDDDMACHK---
                                                                                                   -ACHKIPVEADFLYAYSTAPGYYSWRNSKDGSWFIQSLCAMLKQYADKLEFMHILTRVNR 241
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 IPVEADFLYAYSTAPGYYSWRNSKDGSWFIQSLCAMLKQYADK-LEFMHILTRVNRKVAT
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Pred. No. 2.1e-33;
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Pred. No. 1.1e-33;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           GenCore version 5.1.3 Copyright (c) 1993 - 2002 Compu
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/SIDS2/gcgdata/geneseq/geneseqp-embl/AA1981.DAT:*
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/SIDS2/gcgdata/geneseq/geneseqp-embl/AA1983.DAT:*
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/SIDS2/gcgdata/geneseq/geneseqp-emb1/AA1998.DAT:*
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aue	AAY21720	20	293	35.9	525.5
9.8	AA021924	23	276	36.0	526
Recombinant CPP-32	AAU79218	21	107	7	551
interl	AAR95830	17	341	9.	582
nid	AAB98655	22	244	9.	723.5
pase 7	ABB09300	23	336	49.6	725
caspase 7	ABB09299	23	303	49.6	725
Human caspase 7 pr	ABB09297	23	303		725
Human caspase-7 SE	ABJ01222	23	303		725
Human caspase-7.	AAE00604	22	303	49.6	725
Ļ.	AAY21721	20	303	9.	725
	AAW15262	18	303	49.6	725
ine proteas	AAW15247	18	303	9.	725
7	ABB09298	23	340	۲.	748.5
Mouse caspase 7 pr	ABB78588	23	303	1.	748.5
HER2	ААВ82925	22	527		766.5
HER2	AAB82924	22	513	۲,	766.5
Amino acid sequenc	ABB09606	23	182	σ,	833
Human uncleavable	ABJ01227	23	285	61.2	896
o acid sequ	AAY21726	20	. 285	61.2	896
	AAU80040 .	22	556	Η.	900
angec	AAU97935	22	556	61.5	900
Human milk fat glo	AAU80335	22	559	2	912
Fab/C	AAU80038	22	559	۶	912
Fab1	AAU97946	22	559		912
Rev-c	АВJ01226	23	290	٢	912
Į,	AAY21725	20	290	۲,	912
ic cas	AAE00610	22	261	5	1271.5
se-3	AAB98654	22	241	7.	1281
n caspase-	AAB59579	22	245	7.	1286.5
se caspase 3.	AAU05395	22	277		1293
o o	AAG78712	22	277		1296
interleukin-	AAW47089	19	277		1304
caspase	AAB26763	21	249	90.4	1322
Mutant human apopa	9	19	277		1453

ALIGNMENTS

RESULT 1 AAW00372

AAW00372 standard; protein; 277

AA

26-JUN-1997 AAW00372;

(first entry)

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CPP23beta; isoform; inactive; CPP32; proenzyme; cysteine; protease; proteolytic product; poly(DP-ribose) polymerase; PARP; apopain; cleavage enzyme; human; monocytic leukaemia; cell line; THP-1; identification; modulator; recombinant production; gene therapy; pro-inflammatory; pro-apoptotic; apoptosis; inflammation; antibody; antisense DNA; treatment; immunne; proliferation; degeneration; disease; AIDS; acquired immunodeficiency syndrome; autoimmune; pathogenic infection; cardiovascular; neurological; injury; alopecia; ageing; cancer; type I diabetes; Parkinson's;
                                                                                                             Key
Domain
 Cleavage-site
                                                                   Cleavage-site
Region
                            Protein'
                                                                                                                                                      Homo sapiens
                                                                                                                                                                                                                                                                                                                                     Apopain CPP32beta proenzyme.
29..175
/note= "17 kDa subunit p17"
175..176
                                                                   /note=
28..29
29..46
                                                                                                                          Location/Qualifiers
                                                      /note=
                                       "amino-terminal sequence determined purified enzyme subunits"
                                                                                               "amino-terminal pro-domain"
                                                        for
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AAE00600 ABJ01218

Human caspase-3. Human caspase-3 SE Human caspase

apopa

AAW48945

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The present sequence is the CPP23beta or Glu190 isoform of the inactive CPP32 proenzyme (a member of the interleukin converting CC inactive CPP32 proenzyme (a member of the interleukin converting CC enzyme/pro-apoptotic protein CED-3 family of cysteine proteases of CC unknown function cloned from Jurkat cells), the proteolytic product CC of which is the polytop-ribose) polymerase (PARP) protease.

CC apopain. The PARP cleavage enzyme was purified from the human CC monocytic leukaemia cell line, THP-1, using standard ion exchange CC correct corr
                                                                                                                                                                                                                                                                                                                                                                           Best Loc
Matches
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                                                                                                                                                                                                                                                                                                                                                                                                                                                           Sequence
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               proteolytic broccurs at the
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Apopain, a new human apoptosis related enzyme - responsible for the proteolytic breakdown of poly(ADP- ribose) polymerase (PARP) which
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 (MERI
                                                  181
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                                                                                                                                                                                                                                                                                                      1 MENTENSVDSKSIKNLEPKIIHGSESMDSGISLDNSYKMDYPEMGLCIIINNKNFHKSTG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ary, alopecia, ageing
Alzheimer's disease.
RKVATEFESFSFDATFHAKKQIPCIVSMLTKELYFYH
                                   DWACHKIPVEADFLYAYSTAPGYYSWRNSKDGSWFIQSLCAMLKQYADKLEFMHILTRVN
                                                    DMACHKIPVEADFLYAYSTAPGYYSWRNSKDGSWFIQSLCAMLKQYADKLEFMHILTRVN
                                                                                                                                    HGEEGIIFGTNGPVDLKKITNFFRGDRCRSLTGKPKLFIIQACRGTELDCGIETDSGVDD
                                                                                                                                                                                               MTSRSGTDVDAANLRETFRNLKYEVRNKNDLTREEIVELMRDVSKEDHSKRSSFVCVLLS
                                                                                                                                                                                                                    MTSRSGTDVDAANLRÉTFRNLKYEVRNKNDLTREEIVELMRDVSKEDHSKRSSFVCVLLS 120
                                                                                                                 HGEEGIIFGTNGPVDLKKITNFFRGDRCRSLTGKPKLFIIQACRGTELDCGIETDSGVDD
                                                                                                                                                                                                                                                                                 MENTENSVDSKSIKNLEPKIIHGSESMDSGISLDNSYKMDYPEMGLCIIINNKNFHKSTG
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MERCK FROSST CANADA INC.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                         277 AA;
                                                                                                                                                                                                                                                                                                                                                                         Conservative
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                                                                                                                                                                                                                                                                                                                                                                       0
                                                                                                                                                                                                                                                                                                                                                              Score 1463; DB 17;
Pred. No. 1e-147;
; Mismatches 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         pentapeptide containing putative
cysteine"
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  277
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AAW00677
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Best Local S
Matches 277
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Human pro-Yama (AAW00677) is a zymogen which upon activation cleaves PARP to an 85 kDa form. Activated Yama has the ability to modulate cellular function associated with the Fas receptor pathway such as Fas-associated apoptosis. This activity is inhibited by CrmA (see also AAW00678). The pro-Yama sequence was deduced from a cDNA clone isolated from human umbilical vein endothelial cells. Yama can be produced in a host cell and used to modulate cellular function, to raise antibodies, or to screen for agents or drugs which modulate
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            New nucleic acid encoding Yama protein or CrmA mutant -modulating apoptosis, maintaining {\tt T} cell viability in Al and for drug screening
                181
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13-FEB-1995;
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DMACHKIPVEADFLYAYSTAPGYYSWRNSKDGSWFIQSLCAMLKQYADKLEFMHILTRVN
                                                                                                                                HGEEGIIFGTNGPVDLKKITNFFRGDRCRSLTGKPKLFIIQACRGTELDCGIETDSGVDD
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277; Conserv
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95US-0389812.
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Pred. No. 1e-147;
Mismatches (
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                                                                                                                                                                                                                                                                                                      This ICE-LAP-4 protein may be used therapeutically, e.g. as an antitumor or antiviral agent and to control embryonic development and tissue homeostasis. The protein can also be used to treat immunosuppression disorders, such as AIDS, by targeting virus infected cells for cell death. The DNA may find use in gene
                                                                                                                                                                                                                                                                                                                                                                                                   Human ICE-LAP-3 and -4 DNA and protein - useful in the diagnosis and treatment of Alzheimer's disease, Parkinson's disease, rheumatoid arthritis, septic shock and head injury
                                                                                                                                                                                                                                                                          Sequence
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enzyme: Alzheimer's disease; Parkinson's disease; septic shock;
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              241
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                                                                                           121 HGEEGIIFGTNGPVDLKKITNFFRGDRCRSLTGKPKLFIIQACRGTELDCGIETDSGVDD 180
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                                                                                                                                                                                         MENTENSYDSKSIKNLEPKIIHGSESMDSGISLDNSYKMDYPEMGLCIIINNKNFHKSTG 60
             RKVATEFESFSFDATFHAKKQIPCIVSMLTKELYFYH
                                MTSRSGTDVDAANLRETFRNLKYEVRNKNDLTREEIVELMRDVSKEDHSKRSSFVCVLLS
                                                                                                                                                                            MENTENSVDSKSIKNLEPKIIHGSESMDSGISLDNSYKMDYPEMGLCIIINNKNFHKSTG
                                                                                                                             MTSRSGTDVDAANLRETFRNLKYEVRNKNDLTREEIVELMRDVSKEDHSKRSSFVCVLLS
                                                                               HGEEGIIFGTNGPVDLKKITNFFRGDRCRSLTGKPKLFIIQACRGTELDCGIETDSGVDD
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         injury;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  applications.
                                                                                                                                                                                                                                        Similarity
                                                                                                                                                                                                                                                                          277 AA;
                                                                                                                                                                                                                           Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              (first
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         rheumatoid arthritis
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      He W,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             GENOME SCI INC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    94US-0334251
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            95WO-US07235
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Protein;
                                                                                                                                                                                                                                     100.0%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Hudson PL,
                                                                                                                                                                                                                           0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           277
                                                                                                                                                                                                                                    Score 1463; DB 1
Pred. No. 1e-147;
                                                                                                                                                                                                                          Mismatches
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Rosen CA;
                                                                                                                                                                                                                                                DB 17;
                                                                                                                                                                                                                          0;
                                                                                                                                                                                                                           Indels
                                                                                                                                                                                                                                               Length 277;
                                                                                                                                                                                                                         0;
                                                                                                                                                                                                                         Gaps
                                                                                                                             120
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61 61 ₽ δÃ

MTSRSGTDVDAANLRETFRNLKYEVRNKNDLTREEIVELMRDVSKEDHSKRSSFVCVLLS 120

MTSRSGTDVDAANLRETFRNLKYEVRNKNDLTREEIVELMRDVSKEDHSKRSSFVCVLLS

120

60 60

Query Match Best Local 9 Matches

Similarity

100.0%;

Score 1463; DB 19; Length 277; Pred. No. 1e-147;

Conservative

0;

Mismatches

0;

Indels

0;

Gaps

0

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181 181 121 121

240

240

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241
RKYATEFESFSFDATFHAKKQIPCIYSMLTKELYFYH
 277
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RESULT 4
AAW41688
designated YAMA. The specification describes a novel method of controlling cell functions controlled by the tumour necrosis factor receptor (TNF-R) pathway containing U1-70. The method comprises introducing a nucleic acid molecule encoding CrmA into a cell, and culturing the cell under suitable conditions for transcription and translation of the CrmA nucleic acid. Method for preventing and inhibiting apoptosis by inhibiting activation of the U1-70 path, identifying the chemical related to the apoptosis path, and screening candidate chemical having biological function in the apoptosis path a also described. The methods can be used to identify substances which modulate apoptosis in cells controlled by the TNF-R pathway.
                                                                                                                                                                                                                                                         Controlling apoptosis by inhibiting activation of the U1-70 pathway - by introduction of nucleic acid encoding protein with CrmA biological activity into the cell
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  CrmA; tumour necrosis factor receptor; TNF-R; U1-70; apoptosis; activation; U1-70 path; apoptosis path; id
Sequence
                                                                                                                                                                                                                            Disclosure; Fig 2; 48pp; Japanese.
                                                                                                                                                                                                                                                                                                                      N-PSDB;
                                                                                                                                                                                                                                                                                                                                                                                                 09-FEB-1996;
                                                                                                                                                                                                                                                                                                                                                                                                                               27-JAN-1997;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Synthetic.
                                                                                                                                                                                                                                                                                                                                                                                                                                                             25-NOV-1997.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           JP09299077-A
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     modulation.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             02-JUL-1998
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             AAW41688
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        AAW41688 standard; Protein;
                                                                                                                                                                                                                                                                                                                                                                 (UNMI ) UNIV MICHIGAN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Amino acid sequence of a protein designated YAMA
                                                                                                                                                                                                                                                                                                                     1998-056551/06
DB; AAV05471.
277 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             (first
                                                                                                                                                                                                                                                                                                                                                                                                 96US-0591605
                                                                                                                                                                                                                                                                                                                                                                                                                               97JP-0012932
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             entry)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  0; inhibition;
identification;
                                                                       screening
                                                          are
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RESULT 5
AAW16600
ID AAW16600
ID AAW16600
ID AAW16600
ID AAW1600
ID AAW16600
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The present sequence is the CPP23a or Asp190 isoform of the inactive CPP32 proenzyme (a member of the interleukin converting enzyme/pro-apoptotic protein CED-3 family of cysteine proteases cunknown function cloned from Jurkat cells), the proteolytic prod of which is the poly(DP-ribose) polymerase (PARP) protease,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            CPP23a; isoform; inactive; CPP32; proenzyme; cysteine; protease; proteolytic product; poly(DP-ribose) polymerase; PARR; apopain; cleavage enzyme; human; monocytic leukaemia; cell line; THP-1; identification; modulator; recombinant production; gene therapy; pro-infiammatory; pro-apoptotic; apoptosis; inflammation; antibody; antisense DNA; treatment; immune; proliferation; degeneration; disease; AIDS; acquired immunodeficiency syndrome; autoimmune; pathogenic infection; cardiovascular; neurological; injury;
                                                                                                                                                                                                             Apopain, a new human apoptosis related enzyme proteolytic breakdown of poly(ADP- ribose) pol
                                                                                                                                                 Claim 1;
                                                                                                                                                                                                                                                                                                                                         Ali A,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    17-APR-1996;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Protein
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    24-OCT-1996
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Region
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Cleavage-site
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Domain
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Homo sapiens
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       26-JUN-1997
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                lopecia; ageing; cancer; type I diabetes; Parkinson's
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       241
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                                                                                                                                                                                                                                                                                                                                                                                    MERCK
                                                                                                                                                                                                                                                                                                                                                                                                             MERCK
                                                                                                                                              Page -; 84pp; English.
                                                                                                                                                                                          the onset of apoptosis
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                                                                                                                                                                                                                                                                                                                                                                                    FROSST CANADA INC.
                                                                                                                                                                                                                                                                                                                                                                                                             & CO INC
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175..176
176..193
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28..29
29..46
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      176..277
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                /note-
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              protein;
                                                                                                                                                                                                                                                                                                                                      Nicholson DW,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         "17 kDa subunit
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               "amino-terminal
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              "amino-terminal pro-domain"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           "12 kDa subunit p12"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               "conserved
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         catalytic
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     purified
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              277 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       enzyme
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         pentapeptide containing putative
cysteine"
                                                                                                                                                                                                                                                                                                                                 Thornberry NA,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         p17"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          sequence determined
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       subunits"
                                                                                                                                                                                                             yme - responsible polymerase (PARP)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  277
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                                                                                                                                                                                                                                                                                                                               Vaillancourt JP;
                                                                                                                                                                                                                (PARP)
                                                                                                                                                                                                                ) which
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RESULT 6
AAY21717
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Best Local S
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                                                                                                                                                                                                                                  Rev-caspase; cysteine protease; zymogen; caspase; autoimmune disease; caspase-mediated apoptosis; ne tumour cell; myocardial infarction; human.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        apopain. The PARP cleavage enzyme was purified from the human monocytic leukaemia cell line, THP-1, using standard ion exchange chromatography techniques and SDS PAGE. Apopain can be used to identify apopain activity modulators, while apopain encoding DNA may be used for apopain production or in gene therapy (i.e. in vivo or ex vivo gene transplantation) for enhancing the pro-inflammatory or pro-apoptotic effects of apopain. Anti-apopain antibodies and antisense DNA can be used to reduce or eliminate the
                                                   Alnemri ES;
                                                                                                    09-JAN-1998;
                                                                                                                                                                                 W09935277-A2
                                                                                                                                                                                                            Homo
                                                                                                                                                                                                                                                                                     Amino acid sequence
                                                                                                                                                                                                                                                                                                                                                                   AAY21717 standard; Protein; 277
                                                                          (UYJE-) UNIV
                                                                                                                              11-JAN-1999;
                                                                                                                                                        15-JUL-1999
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  pro-inflammatory or pro-apoptotic effects of apopain. Modulation of apopain activity is beneficial in the treatment of immune, proliferative and degenerative diseases, e.g. AIDS, autoimmune
                                                                                                                                                                                                                                                                                                                  10-SEP-1999
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                injury, alopecia, ageing, cancer, type I diabetes and Parkinson's and Alzheimer's disease.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        disease, pathogenic infections, cardiovascular and neurological
                                                                                                                                                                                                                                                                                                                                                                                                                                      241
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                                                                                                                                                                                                                                                                                                                                                                                                                                               RKVATEFESFSFDATFHAKKQIPCIVSMLTKELYFYH 277
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                                                                                                                                                                                                                                                                                                                                                                                                                                     RKVATEFESFSFDATFHAKKQIPCIVSMLTKELYFYH
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       DMACHKIPVDADFLYAYSTAPGYYSWRNSKDGSWFIQSLCAMLKQYADKLEFMHILTRVN
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                                                                          JEFFERSON THOMAS
                                                                                                    98US-0070987
                                                                                                                              99WO-US00632
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       AA;
                                                                                                                                                                                                                                                                                     of caspase-3 (CPP32).
                                                                                                                                                                                                                                                                                                               entry)
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99.6%;
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                                                                                                                                                                                                                                                            cancer;
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                                                                                                                                                                                                                                                            gene therapy;
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WPI; 1999-419353/35 N-PSDB; AAX81219.

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RESULT 7
AAU05394
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Best Local (
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Cells transfected with a rev-caspase expressing vector can be used in identification of inhibitors or enhancers of caspase-mediated apoptosis. In vitro translated rev-caspase can be used to identify an inhibitor or enhancer of caspase processing activity. Caspase inhibitors are useful for treating neurodegenerative diseases as well as for inhibiting apoptosis in the heart following myocardial infarction. Sequences AAX81217 -AAX81226 represent human caspase genes encoding caspase 1-10 gene products (AAY21715-Y21724).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Rev-caspases are cysteine proteases that specifically cleave proteins after Asp residues and is expressed as a zymogen, in which the small subunit is N-terminal to a large subunit. A gene delivery vehicle comprising a rev-caspase coding sequence is useful for the treatment of cancer, where the gene delivery vehicle is internalised by tumour cells. The gene delivery vehicle can also be used to treat autoimmune diseases.
                                                                                                                                                                       Human; caspase 3; viral infection; l
                                                                                                                                                                                                                                                                                                         AAU05394 standard;
            18-JAN-2000; 2000US-0484617
                                       11-JAN-2001; 2001WO-US00888
                                                                                                 WO200153310-A1
                                                                                                                              Homo sapiens
                                                                                                                                                           atherosclerosis;
                                                                                                                                                                                                                  Human caspase
                                                                                                                                                                                                                                                  24-OCT-2001
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          cancer
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     New isolated nucleic acid molecule encoding a rev-caspase - used for screening and identifying inhibitors or enhancers for treating
                                                                                                                                                                                                                                                                                                                                                                                     241
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      MENTENSVDSKSIKNLEPKIIHGSESMDSGISLDNSYKMDYPEMGLCIIINNKNFHKSTG 60
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  l Similarity
276; Conserv
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                                                                                                                                                        ; apoptosis; hyperproliferative disorder; hepatitis;
haematopoietic disorder; autoimmune disorder;
neurological disorder.
                                                                                                                                                                                                                                                                                                          Protein; 277
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             to nucleic acid molecules encoding rev-caspases
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Pred. No. 2.2e-147;
1; Mismatches 0;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     in an invention relating to novel antisense oligonucleotides (AASI0617-AASI0676) and methods of using these compounds for the modulation of caspase 3 expression. The caspase 3 antisense oligonucleotides specifically hybridise with and inhibit the expression of caspase 3. Antisense compounds targeted to caspase 3 are useful to inhibit caspase 3 expression in cells or tissues and to modulate apoptosis. The caspase 3 antisense oligonucleotides are useful for treating disorders associated with expression of caspase 3.
                                                                                                                                                                           Human; caspase-3; CPP32; yama; apopain; cysteine protease; apoptosis; caspase expression cassette; metastasis; tumour; cathepsin B; urokinase; proliferation; gene therapy.
                                               Cleavage-site
                                                                                                                                                                                                                                                                                               Human caspase-3
                                                                                                                                                                                                                                                                                                                                                                                                          AAE00600;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                  AAE00600 standard; Protein;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Such disorders include hyperproliferative disorders (e.g. cancer), viral infections (e.g. hepatitis), haematopoietic disorders, autoimmune disorders, atherosclerosis and neurological disorders (e.g. Alzheimer's
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    The
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DB; AAS10503.
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276; Conserv
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Conservative
                                                                                                                                                                                                                                                                                                                                                    (first entry)
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                                               Location/Qualifiers
9..10
/label= Proteolytic_cleavage_site
28..29
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..2e-147;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     CC CP932, yama and apopain. Caspases are a family of cysteine proteases, ct that participate in the initiation and execution of apoptosis. Caspases ce exist as pro-enzymes, activated by cleavage into a large and small correctly pro-enzyme sequence. The present invention relates to a method for curional cloning of genes encoding proteins or enzymes involved in correctly cleavage. The invention is based on the use of caspase expression cassettes comprising the coding sequence of a proteolytic cleavage in the invention is based on the use of caspase expression cassettes comprising the coding sequence of a proteolytic cleavage site flanked by sequences encoding two caspase subunit. A cc cleavage site flanked by sequences encoding two caspase subunit, and company of the comprising a first and a second caspase subunit. Cc cleavage site containing a first and a second caspase subunit, and company of the containing gene encoding enzymes involved in proteolytic cleavage. An occ mutant cell line deficient in an enzyme of interest and is also useful cc call genes and caspase subunity a mutant cell line deficient in an enzyme of interest and is also useful company of the containing fusion polypeptide (e.g. Cathepsin B course) is used to interest and is also useful contained by overexpression of a polypeptide (e.g. Cathepsin B course) is used to interest and is also useful contained by a case of the containing fusion polypeptide (e.g. Cathepsin B course) is used to interest and is also useful contained by a case of the course of the contained by a case of the containing fusion polypeptide (e.g. Cathepsin B course) is used to interest and is also useful contained by a case of the course of the course c
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              fusion polypeptide is used
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      241
                                               241
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14-AUG-2000;
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RKVATEFESFSFDATFHAKKQIPCIVSMLTKELYFYH
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                           RKVATEFESFSFDATFHAKKQIPCIVSMLTKELYFYH 277
                                                                                 DMACHKIPVDADFLYAYSTAPGYYSWRNSKDGSWFIQSLCAMLKQYADKLEFMHILTRVN
                                                                                                  DMACHKIPVEADFLYAYSTAPGYYSWRNSKDGSWFIQSLCAMLKQYADKLEFMHILTRVN
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DB; AAD03910.
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                                                                                                                                                                                                                                                                                                                                                                                                                        276;
                                                                                                                                                                                                                                                                                                                                                                                                                                       Similarity
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                                                                                                                                                                                                                                                                                                                                                                                                                      Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            in gene therapy.
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Pred. No. 2.2e
1; Mismatches
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2.2e-147;
nes 0;
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RESULT

RESULT 10
AAW48945
ID AAW48
XX

AAW48945

standard;

Protein;

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ABJ01218
ID ABJ0
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AC ABJ0
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DE Huma
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KW Huma
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OS Homo
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VS63
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PR 09-J
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Matches 276
                                                                                                                                                                                                                                                                                                           The present invention provides the protein and coding sequences of human rev-caspase-3, uncleavable rev-caspase-3 and rev-caspase-6. The sequences can be used in the gene therapy of cancer and autoimmune diseases. The present sequence is a protein described in the exemplification of the
                                                                                                                                                                                                                                                                             Sequence
                                                                                                                                                                                                                                                                                                                                                                     Disclosure;
                                                                                                                                                                                                                                                                                                                                                                                                      New rev-caspases engineered to contain the small subunit fused in N-terminal to the large subunit, which is in reverse order to the
                                                                                                                                                                                                                                                                                                                                                                                                                                        N-PSDB;
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08-JAN-1999;
                                                                                                                                                                                                                        Local 276;
                                                                                                                                                                                                                                                                                                   invention
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Human; caspase;
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                                                                                                                                                                                             1 MENTENSVDSKSIKNLEPKIIHGSESMDSGISLDNSYKMDYPENGLCIIINNKNFHKSTG
          RKVATEFESFSFDATFHAKKQIPCIVSMLTKELYFYH 277
                                        HGEEGIIFGTNGPVDLKKITNFFRGDRCRSLTGKPKLFIIQACRGTELDCGIETDSGVDD 180
                                                                                                                                  MTSRSGTDVDAANLRETFRNLKYEVRNKNDLTREEIVELMRDVSKEDHSKRSSFVCVLLS 120
RKVATEFESFSFDATFHAKKQIPCIVSMLTKELYFYH
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                                                                                                                                                                                                                                                                                                                                                                                           caspases, are useful
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                                                                                                                                                                                                                                          Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                caspase; rev-caspase; gene therapy; protease; apoptosis;
autoimmune disease; cytostatic; immunosuppressive.
                                                                                                                                                                                                                                                                             277
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                                                                                                                                                                                                                                Conservative
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99US-0227721.
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                                                                                                                                                                                                                             Score 1460; D
Pred. No. 2.2e
1; Mismatches
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                                                                                                                                                                                                                                                                                                                                                                                           treat cancer and autoimmune diseases
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2.2e-147;
277
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                                                                                                                                                                                                                                                                                                                               alkylating agents. The mutation affects the catalytic properties of the enzyme but does not affect their binding properties. The invention provides for new ligands for use in SPA which have increased binding affinity for a tyrosine phosphatase or cysteine protease. The ligands contain at least two 4-phosphono(difluoromethyl) phenylalanine groups which increase binding affinity of the ligand to its respective enzyme. The assay can be used to determine the ability of new ligands and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Enzyme binding assay for detection of useful compounds - use form of wild-type enzyme, in which serine replaces cysteine active site, to reduce interference from oxidising/alkylatir
                                                                                                                                                                                                                                                         compound mixtures to competitively bind with an enzyme. The method is claimed to allow a better usage of SPA in the discovery of compounds the treatment and study of diseases, e.g. diabetes, cancer and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  using mutated proteases and phosphatases whereby the catalytic cysteine residue of the enzymes are replaced with a serine or alanine residue to correct the problem of interference in SPA from extraneous oxidising and correct the problem of interference in SPA from extraneous oxidising and correct the problem of interference in SPA from extraneous oxidising and correct the problem of interference in SPA from extraneous oxidising and correct the problem of interference in SPA from extraneous oxidising and correct the problem of interference in SPA from extraneous oxidising and correct the problem of interference in SPA from extraneous oxidising and correct the problem of interference in SPA from extraneous oxidising and correct the problem of interference in SPA from extraneous oxidising and correct the problem of interference in SPA from extraneous oxidising and correct the problem of interference in SPA from extraneous oxidising and correct the problem of interference in SPA from extraneous oxidising and correct the problem of interference in SPA from extraneous oxidising and correct the problem of interference in SPA from extraneous oxidising and correct the problem of interference in SPA from extraneous oxidising and correct the problem of interference in SPA from extraneous oxidising and correct the problem of interference in SPA from extraneous oxidising and correct the problem of interference in SPA from extraneous oxidising and correct the problem of interference in SPA from extraneous oxidising and correct the problem of interference in SPA from extraneous oxidising and correct the problem of interference in SPA from extraneous oxidising and correct the problem of interference in SPA from extraneous oxidising and correct the problem of interference in SPA from extraneous oxidising and correct the problem of interference in SPA from extraneous oxidising and correct the problem of interference in SPA from extraneous oxidising and correct the correct the correct the correct the correct that the correct the 
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   The invention claims for a method for use in a scintillation binding assay (SPA) for proteases and phosphatases. The method to use in a scintillation
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           The present sequence represents a mutated human apopain (caspase-3) C163S pro-enzyme. The active enzyme containing P17 subunit (Ser29-Asp175) and P12 subunit (Ser176-His277) was engineered for expression using the MetSer29-Asp175 and MetSer176-His277 constructs. The invention claims for a method for use in a scintillation proximit
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Disclosure; Pages 39-40; 63pp; English.
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                                                                                                                                                                                      Sequence
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Kennedy B,
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                        1 MENTENSVDSKSIKNLEPKIIHGSESMDSGISLDNSYKMDYPEMGLCIIINNKNFHKSTG
1 Similarity
276; Conser
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       s S, Ford-Hu
B, Nicholson
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163
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176..277
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Pred. No. 1.2e
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dran C,
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The present sequence represents a mutated human apopain (caspase-3) C163S pro-enzyme. The active enzyme containing P17 subunit (Ser29-Asp175) and P12 subunit (Ser176-His277) was engineered for expression using the MetSer29-Asp175 and MetSer176-His277 constructs. The invention provides a method for use in a scintillation proximity binding assay (SPA) for proteases and phosphatases. The method invol
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Mutant human apopain pro-enzyme; caspase-3 scintillation proximity binding assay; dia 4-phosphono(difluoromethyl) phenylalanine
                                                                                                             Peptide(s) useful in binding assays for tyrosine phosphatases or cysteine proteases - contain two or more 4-phosphono(difluoromethyl) phenylalanine groups to improve binding affinity
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                                                                                      Disclosure;
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mutant"
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ine group; osteoporosis;
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The method involves

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RESULT 12
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Best Local S
Matches 276
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         residue of the enzymes are replaced with a serine or alanine residue to correct the problem of interference in SPA from extraneous oxidising and alkylating agents. The mutation affects the catalytic properties of the enzyme but does not affect their binding properties. The invention claims for new ligands for use in SPA which have increased binding affinity for a tyrosine phosphatase or cysteine procease. The ligands contain at least two 4-phosphono(difluoromethyl) phenylalanine groups which increase binding affinity of the ligand to its respective enzyme. The assay can be used to determine the ability of new ligands and compound mixtures to competitively bind with an enzyme. The method is claimed to allow a better usage of SPA in the discovery of compounds for the treatment and study of diseases, e.g. diabetes, cancer and
     Judgement of apoptosis-controlling activity for selecting drugs can be \mu sed for preventing and treating various diseases caused abnormality in apoptosis control -
                                                                                                                                                                                                                                                                                                          Human caspase-1
                                                                                                                                                                                                                                                                                                                                                                                           AAB26763 standard;
                                                                    WPI; 2000-605051/58
                                                                                                                          29-JAN-1999;
                                                                                                                                                    29-JAN-1999;
                                                                                                                                                                                                             JP2000217598-A
                                                                                                                                                                                                                                        Homo sapiens
                                                                                                                                                                                                                                                                   caspase;
                                                                                                                                                                                                                                                                             Apoptosis; detection; Nrf2;
                                                                                                                                                                                                                                                                                                                                       16-JAN-2001
                                                                                             (SUMO ) SUMITOMO CHEM
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    osteoporosis.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      MENTENSYDSKSIKNLEPKIIHGSESMDSGISLDNSYKMDYPEMGLCIIINNKNFHKSTG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                              RKVATEFESFSFDATFHAKKQIPCIVSMLTKELYFYH 277
                                                                                                                                                                                                                                                                                                                                                                                                                                                                 RKVATEFESFSFDATFHAKKQIPCIVSMLTKELYFYH
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   DMACHKIPVEADFLYAYSTAPGYYSWRNSKDGSWFIOSLCAMLKQYADKLEFMHILTRVN 240
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             HGEEGIIFGTNGPVDLKKITNFFRGDRCRSLTGKPKLFIIQASRGTELDCGIETDSGVDD
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           HGEEGIIFGTNGPVDLKKITNFFRGDRCRSLTGKPKLFIIQACRGTELDCGIETDSGVDD
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                MTSRSGTDVDAANLRETFRNLKYEVRNKNDLTREEIVELMRDVSKEDHSKRSSFVCVLLS 120
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      DMACHKIPVEADFLYAYSTAPGYYSWRNSKDGSWFIQSLCAMLKQYADKLEFMHILTRVN
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276; Conser
                                                                                                                                                                                                                                                                   cancer;
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                                                                                                                                                                                                                                                                                                                                   (first entry)
                                                                                                                        99JP-0022356
                                                                                                                                                    99JP-0022356
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         AA;
                                                                                                                                                                                                                                                                                                       protein sequence
                                                                                                                                                                                                                                                                    human
                                                                                                                                                                                                                                                                                                                                                                                           protein;
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                                                                                             CO LTD
                                                                                                                                                                                                                                                                           drug identification; prevention;
                                                                                                                                                                                                                                                                                                                                                                                             249
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Pred. No. 1.2e-146;
0; Mismatches 1;
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                                                                                                                                                                                                                                                                             treatment;
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AAW47
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AAW47089
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Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    A method for identifying drugs which exhibit apoptosis-controlling activity involves the use of a human Nrf2 protein. Nrf2 is a caspase substrate. The method involves detecting cleavage of the Nrf2 protein by caspase in the presence of a candidate drug. Detection of cleavage of the Nrf2 protein by caspase in the presence of a candidate drug indicates apoptosis inducing activity. The method can be used for selecting a drug which can be used for the prevention and the treatment of various diseases caused by abnormality in apoptosis control, such as cancer. The
                       N-PSDB; AAV13959
                                                                                                                                                                                                                                                                Interleukin-1 beta converting enzyme related protease; ICE related protease; rat; apoptosis; inhibitor; brain ischaemia; Alzheimer's disease; amyotrophic lateral sclerosis; head trauma;
                                                                                                                                                                                                                                                                                                                                                                                                      AAW47089 standard; Protein; 277
                                                                                        (ELIL ) LILLY &
                                                                                                                    22-JUL-1996;
                                                                                                                                              15-JUL-1997;
                                                                                                                                                                         29-JAN-1998
                                                                                                                                                                                                  WO9803642-A1
                                                                                                                                                                                                                             Rattus
                                                                                                                                                                                                                                                      neurodegenerative
                                                                                                                                                                                                                                                                                                                      Rat interleukin-1 beta converting enzyme-related
                                                                                                                                                                                                                                                                                                                                                  20-JUL-1998
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              present sequence represents the human caspase-1 protein used in the \operatorname{method}.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Claim 5;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                           241
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        29 SGISLDNSYKMDYPEMGLCIIINNKNFHKSTGMTSRSGTDVDAANLRETFRNLKYEVRNK 88
                                    1998-120767/11
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        LTKELYFYH 277
                                                                                                                                                                                                                                                                                                                                                                                                                                                                           LTKELYFYH 249
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             SKDGSWFIQSLCAMLKQYADKLEFMHILTRVNRKVATEFESFSFDATFHAKKQIPCIVSM
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           SKDGSWFTQSLCAMLKQYADKLEFMHILTRVNRKVATEFESFSFDATFHAKKQIPCIVSM
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                RSLTGKPKLFIIQACRGTELDCGIETDSGVDDDMACHKIPVEADFLYAYSTAPGYYSWRN 208
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     NDLTREEIVELMRDVSKEDHSKRSSFVCVLLSHGEEGIIFGTNGPVDLKKITNFFRGDRC 148
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          SGISLDNSYKMDYPEMGLCIIINNKNFHKSTGMTSRSGTDVDAANLRETFRNLKYEVRNK
                                                                                                                                                                                                                             qs
                                                               Paul SM,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Page 13; 17pp;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   249 AA;
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                                                                                                                    96US-0022049
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Pred. No. 1.1e-132;
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Rat interleukin-1 beta converting enzyme related protease -

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RESULT 14
AAG78712
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Best Local S
Matches 245
  (NORQ ) NORINSUISANSHO KACHIKU EISEI.
(MUNE/) MUNETA Y.
(MORI/) MORI Y.
                                                                                   05-OCT-1999;
                                                                                                                                                                                                                                                                                                                                                                                                                           AAG78712;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                    AAG78712 standard;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      be used in a claimed method to identify compounds that inhibit apoptosis. Such inhibitors can be used to treat Alzheimer's disease, amyotrophic lateral sclerosis (ALS), head trauma or other neurodegenerative disorders in humans (all claimed). Antibodies raised against the protease may be usef dor diagnosis of these disease states, or in their treatment.
                                                                                                                          03-OCT-2000; 2000JP-0303931
                                                                                                                                                                                                             JP2001169785-A
                                                                                                                                                                                                                                                    Sus scrofa
                                                                                                                                                                                                                                                                                                                                   Pig caspase
                                                                                                                                                                                                                                                                                                                                                                                 11-DEC-2001
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   rat brain cDNA library. ICE related protease is present in the central neurons system and is enriched in central neurons of the hippocampus including pyramidal neurons are recommended in the hippocampus including pyramidal neurons of the hippocampus pyramidal neurons of the hippocampus pyramidal neurons of the hippocampus pyramidal neurons of the hippo
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                other neurodegenerative disorders
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  treating Alzheimer's disease, amyotrophic lateral sclerosis,
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       related protease in a host cell is claimed.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                MENTENSVDSKSIKNLEPKIIHGSESMDSGISLDNSYKMDYPEMGLCIIINNKNFHKSTG
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                                                                                                                                                                                                                                                                                            caspase;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       RKVAMEFESFSLDATFHAKKQIPCIVSMLTKELYFYH 277
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              DMACHKIPVEADFLYAYSTAPGYYSWRNSKDGSWFIQSLCAMLKQYADKLEFMHILTRVN
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                RKVATEFESFSFDATFHAKKQIPCIVSMLTKELYFYH 277
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                                                                                                                                                                                                                                                                                                                                                                               (first
                                                                                                                                                                                                                                                                                              inflammation;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       AA;
                                                                                   99JP-0284829
                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Protein;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      89.1%;
                                                                                                                                                                                                                                                                                                                                                                               entry)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  English.
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                                                                                                                                                                                                                                                                                              infection
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Score 1304; DB 1
Pred. No. 1e-130;
3; Mismatches 1
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RESULT 15
AAU05395
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Best Local
                                                                                                                                                                                                                       Mouse; caspase 3; apoptosis; hyperproliferative disorder; hepatitis; viral infection; haematopoietic disorder; autoimmune disorder;
Zhang H,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         The present invention provides two versions of a porcine caspase These can be used to control inflammatory reactions to microbial infectious diseases. The present sequence is one version of the provided the present sequence is one version of the present sequence.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            (SHIM/)
(ARAI/)
                                                         18-JAN-2000;
                                                                                      11-JAN-2001; 2001WO-US00888
                                                                                                                    26-JUL-2001.
                                                                                                                                                 WO200153310-A1
                                                                                                                                                                              Mus musculus
                                                                                                                                                                                                            atherosclerosis;
                                                                                                                                                                                                                                                                    Mouse caspase
                                                                                                                                                                                                                                                                                                    24-0CT-2001
                                                                                                                                                                                                                                                                                                                                AAU05395;
                                                                                                                                                                                                                                                                                                                                                            AAU05395 standard; Protein; 277 AA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             1 MENNKTSVDSKSIKTLETKILHGSKSMDSGISLDVSYKMDYPEMGLCIIINNKNFDKNTG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            2001-592539/67.
DB; AAI66510.
                                                                                                                                                                                                                                                                                                                                                                                                                                     RKVAVEFESFSTDSTFHAKKQIPCIVSMLTKELYFYH
                                                                                                                                                                                                                                                                                                                                                                                                                                                                  RKVATEFESFSFDATFHAKKQIPCIVSMLTKELYFYH 277
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        HGEEGIIFGTNGPVDLKKITNFFRGDRCRSLTGKPKLFIIQACRGTELDCGIETDSGVDD 180
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    MACRSGTDVDAANLRETFTNLKYEVRNKNDLTREEILELMHSVSKEDHSKRSSFICVLLS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  MTSRSGTDVDAANLRETFRNLKYEVRNKNDLTREEIVELMRDVSKEDHSKRSSFVCVLLS 120
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          {\tt HGEEGKIFGTNGPVDLKKLTSFFRGDCCRTLTGKPKLFIIQACRGTELDCGIETDSGTED}
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        al Similarity
245; Conserv
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ARAI K.
                           ISIS PHARM INC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Page 16;
Cowsert LM;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Conservative
                                                         2000US-0484617
                                                                                                                                                                                                                                                                                                 (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 AA;
                                                                                                                                                                                                         neurological
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      23pp; Japanese.
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Pred. No. 7.5e
11; Mismatches
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.5e-130;
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WPI; 2001-442252/47

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Best Local Similarity
Matches 240; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                            The present sequence representing mouse caspase 3 is described in an invention relating to novel antisense oligonucleotides (AASI0517-AASI0676) and methods of using these compounds for the modulation of caspase 3 expression. The caspase 3 antisense oligonucleotides specifically hybridise with and inhibit the expression of caspase 3. Antisense compounds targeted to caspase 3 are useful to inhibit caspase 3 expression in cells or tissues and to modulate apoptosis. The caspase 3 antisense oligonucleotides are useful for treating disorders associated with expression of caspase 3. Such disorders include hyperproliferative disorders (e.g. cancer), viral infections (e.g. hepatitis), haematopoietic disorders, autoimmune disorders, atherosclerosis and neurological disorders (e.g. Alzheimer's
                                                                                                                                                                                                                                                                                                                                                                                                          Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Disclosure; Page 96-97; 127pp; English.
New antisense compound to inhibit caspase 3 is useful for treating hepatitis and atherosclerosis -
                                                                                                                                                                                               MENTENSVDSKSIKNLEPKIIHGSESMDSGISLDNSYKMDYPEMGICIIINNKNFHKSTG 60
                                                                                                                                                                                                                                                                                                                                                                                                        277 AA;
                                                                                                                                                                                                                                                                                                                                     88.4%; Score 1293; DB 22; ilarity 86.6%; Pred. No. 1.6e-129; Conservative 20; Mismatches 17;
                                                                                                                                                                                                                                                                                                                                     Indels
                                                                                                                                                                                                                                                                                                                                                                    Length 277;
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Search completed: December Job time: 32.0431 secs 2, 2002, 12:56:04

В Ş В Ş В Ş

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Result
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Maximum Match 100%
Listing first 45 summaries
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Minimum DB seq
Maximum DB seq
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              8
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Sequence:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Perfect score:
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length: 2000000000
                                                                                                                                                                                                Query
Match
                                                                                                                                                                                                                                                   is the number of results predicted by chance to have a ster than or equal to the score of the result being printed, rived by analysis of the total score distribution.
   100.0
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Gapop 10.0 , Gapext 0.5
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  SPTREMBL_21:*
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                                                                                                                                                                                                                                                                                                                                                                                            sp_phage:*
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Q95ND5
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2172.860 Million cell updates/sec
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099m47 mus musculu
09bq67 homo sapien
091889 oncorhynchu
091b66 xenopus lae
091089 mus musculu
093415 gallus gall
035397 rattus norv
                                                                                                                                     Q96an1 homo sapien
Q96kp2 homo sapien
Q95nd5 sus scrofa
Q9qwi4 mus musculu
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077623 ovis aries
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                                                                          Q98ui8 brachydanio
Q9ib65 xenopus lae
088550 rattus norv
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45	44	43	42	41	40	39	38	37	36	35	34	33	32	31	30	29	28	27	26	25	24	23	22	21	20	19	18	17
283	302.5	306.5	306.5	310.5	310.5	324	325	327.5	328.5	349	360	374.5	383.5	404	417	421	421	422	422	422.5	423	431.5	432.5	434	435	436	437.5	484
19.3														27.6														
383	347	826	263	536	268	423	393	452	435	479	417	520	500	403	416	538	496	308	308	476	399	131	482	454	480	454	482	326
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ALIGNMENTS

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Q96AN1
                                                                                                            Query Match 100.0%;
Best Local Similarity 100.0%;
Matches 277; Conservative 0;
                                                                                                                                                                                                           Strausberg R.;
Strausberg R.;
Submitted (NOV-2001) to the EMBL/GenBank/DDBJ databases
EMBL; BC016926; AAH16926.1;
InterPro; IPR002398; ICE.
InterPro; IPR002398; ICE.p10.
InterPro; IPR001309; ICE.p20.
                                                                                                                                                                                                                                                                                                                                                                                                                   Q96AN1;
Q96AN1;
01-DEC-2001
01-DEC-2001
01-MAR-2002
                                                                                                                                 Pfam; PF00655; ICE_P10; 1.
Pfam; PF00656; ICE_P20; 1.
PRINTS; PR00376; IL1BCENZYME.
PROSTIE; PS01122; CASPASE_CYS; UNKNOWN_1.
PROSTIE; PS01121; CASPASE_P10; UKNOWN_1.
PROSTIE; PS50207; CASPASE_P10; 1.
PROSTIE; PS50208; CASPASE_P20; 1.
                                                                                                         Hypothetical protein.
SEQUENCE 277 AA; 31608 MW;
                                                                                                                                                                                                                                                                                                            TISSUE=LYMPH;
                                                                                                                                                                                                                                                                                                                                         NCBI_TaxID=9606;
                                                                                                                                                                                                                                                                                                                                                               Mammalia; Eutheria;
                                                                                                                                                                                                                                                                                                                                                                             Eukaryota; Metazoa;
                                                                                                                                                                                                                                                                                                                                                                                      Homo sapiens (Human)
                                                                                                                                                                                                                                                                                                                                                                                                     Hypothetical
                                                                                                                                                                                                                                                                                                                         SEQUENCE FROM N.A.
1 MENTENSVDSKSIKNLEPKIIHGSESMDSGISLDNSYKMDYPEMGLCIIINNKNFHKSTG 60
                                                                                                                                                                                                                                                                                                                                                                                                    (TrEMBLrel. 19, Created)
(TrEMBLrel. 19, Last sequence update)
(TrEMBLrel. 20, Last annotation update)
1 31.6 kDa protein.
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                                                                                                                                                                                                                                                                                                                                                              Primates; Catarrhini; Hominidae; Homo.
                                                                                                                                                                                                                                                                                                                                                                             Chordata;
                                                     Score 1463; DB 4;
Pred. No. 1.6e-114;
; Mismatches 0;
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                                                                                                         2F35CD3BCF7FF64A CRC64;
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                                                                                                                                                                                   Pfam; PF00655; ICE_p10; 1.
Pfam; PF00656; ICE_p20; 1.
Pfam; PF00656; ICE_p20; 1.
PRINTS; PR00376; IL1BCENZYME.
PROSITE; PS01122; CASPASE_CYS; UNKNOWN_1.
PROSITE; PS01121; CASPASE_HIS; UNKNOWN_1.
PROSITE; PS50207; CASPASE_P10; 1.
PROSITE; PS50208; CASPASE_P20; 1.
SEQUENCE 277 AA; 31642 MW; 6162767B0D2D
                                                                                                                                                                                                                                                          at the N-terminus of the p17 subunit.", Submitted (OCT-2001) to the EMBL/GenBank/DDBJ EMBL; AJ413269; CAC68866.1; Interpro; IPR002398; ICE_D10. Interpro; IPR002138; ICE_D10. Interpro; IPR001399; ICE_D20.
                                                                                                                                                                                                                                                                                                                                                                                                                                                           Q96KP2;
Q96KP2;
01-DEC-2001
01-DEC-2001
                                                                                                                                                                                                                                                                                                                                     SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                  Vallette
                                                                                                                                                                                                                                                                                                                                                                         SEQUENCE FROM
                                                                                                                                                                                                                                                                                                                                                                                                    Eukaryota; Metazoa;
Mammalia; Eutheria;
                                                                                                                                                                                                                                                                                                  Oliver L.J.;
"Control of the activation of the procaspase-3 by a "the N-terminus of the p17 subunit.";

at the N-terminus of the p17 subunit.";
                                                                                                                                                                                                                                                                                                                                                         Submitted
                                                                                                                                                                                                                                                                                                                                                                                           NCBI_TaxID=9606;
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Eukaryota; Me
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MENTENSVDSKSIKNLEPKIIHGSESMDSGISLDNSYKMDYPEMGLCIIINNKNFHKSTG
                                     MTSRSGTDVDAANLRETFRNLKYEVRNKNDLTREEIVELMRDVSKEDHSKRSSFVCVLLS
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Metazoa; Chordata; C
Metazoa; Primates; (
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1 (TremBLrel. 19,
2 (TremBLrel. 20,
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98.2%;
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Last sequence
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                                                                                                                                                Score 1441; D
Pred. No. 1.1e
2; Mismatches
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ches 3;
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i; Hominidae; Homo.
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Best Local
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InterPro; IPR001309; ICE_p20.
Pfam; PP00655; ICE_p10; 1.
Pfam; PF00655; ICE_p20; 1.
Pfam; PF00656; ICE_p20; 1.
PROSITE; PS01122; CASPASE_HIS; UPROSITE; PS01121; CASPASE_P10; IPROSITE; PS01207; CASPASE_P10; PROSITE; PS0208; CASPASE_P20; 1 PROSITE; PS0208; CASPASE_P20; 1 SEQUENCE 277 AA; 31379 MW; 6
                                                                                                            Q9QWI4;
Q9QWI4;
01-MAY-2000
01-MAY-2000
01-JUN-2002
Mus musculus (Mouse).
Eukaryota; Metazoa; Chordata;
Mammalia; Eutheria; Rodentia;
                                                                                      CPP32 apoptotic
                                                                           CASP3
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01-DEC-2001
01-DEC-2001
01-JUN-2002
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"Porcine caspase-3: cloning and its activity during porcine PK15 cells induced by porcine Fas-ligand.";
J. Interferon Cytokine Res. 21:409-415(2001).
EMBL; AB099345; BAB55544.1; -.
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MEDLINE=21334413; PubMed=11440638;
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0 (TrEMBLrel. 13,
2 (TrEMBLrel. 21,
                                                                                                                                                                                                    PRELIMINARY;
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(TrEMBLrel. 19,
(TrEMBLrel. 21,
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                                                                                        (Fragment).
                                                                                                            Last sequence up
                                                                                                                                                      Created)
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Pred. No. 1.5e
11; Mismatches
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Last sequence
Last anno
  Craniata; Veri
Sciurognathi;
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    Vertebrata; Euteleostomi;
thi; Muridae; Murinae; Mus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     1.5e-100;
nes 21;
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Sus.
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Best Local Similarity
Matches 191; Conserv
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InterPro; IPR002138; ICE_p10.
InterPro; IPR001309; ICE_p20.
Pfam; PF00655; ICE_p10; 1.
Pfam; PF00656; ICE_p20; 1.
Pfam; PF00676; ILBGENZYME.
SWART; SM00115; CASC; 1.
                                                                                                                                                                                             O93417;
01-NOV-1998 (TrEMBLrel.
01-NOV-1998 (TrEMBLrel.
01-MAR-2002 (TrEMBLrel.
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SEQUENCE FROM N.A.
SEQUENCE FROM N.A.
MEDLINE=20149872; PubMed=10684799;
Johnson A.L., Bridgham J.T.;
Johnson A.L., Bridgham J.T.;
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 InterPro; IPR002398;
InterPro; IPR002138;
InterPro; IPR001309;
                              Biol. Reprod. 62:589-598(2000).
EMBL; APO83029; AAC32602.1; -.
HSSP; P42574; IPAU
MEROPS; C14.003; -.
                                                                                                                                                                            Gallus gallus (Chicken).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Protease.
                                                                                                                                                      Eukaryota; Metazoa; Chordata; (Archosauria; Aves; Neognathae;
                                                                                                                                                                                       Caspase-3
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PROSITE; PSO1121; CASPASE_HIS;
PROSITE; PS50207; CASPASE_P10;
PROSITE; PS50208; CASPASE_P20;
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Fortin J.-P., Sekaly R.-P.;
"Multiple Pathways of Apoptosis Converging on the CPP32
Submitted (JUL-1996) to the EMBL/GenBank/DDBJ databases
                                                                        cells."
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                MEROPS; C14.003; -. MGD; MGI:107739; Casp3
                                                                                                                                    NCBI_TaxID=9031;
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HSSP; P42574; 1PAU.
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ICE_p10.
ICE_p20.
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Pred. No. 2.9e
L8; Mismatches
                                                                                                                                                    Craniata; Vertebrata; Euteleostomi;
; Galliformes; Phasianidae; Phasianinae;
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DR Interpro; IPR002138; ICE_p10.
DR Pfam; PF00655; ICE_p20; 1.
DR Pfam; PF00655; ICE_p20; 1.
DR Pfam; PF00656; ICE_p20; 1.
DR PARNTS; PF00376; ILIBCENZYME.
NR SMART; SM00115; CASC; 1.
NR PROSITE; PS01122; CASPASE_CYS; 1.
R PROSITE; PS01121; CASPASE_HIS; 1.
R PROSITE; PS50207; CASPASE_HIS; 1.
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R PROSITE; PS50208; CASPASE_P10; 1.
PROSITE; PS50208; CASPASE_P20; 1.
NON_TER
SEQUENCE 182 AA; 20408 M3: ---
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Best I
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            077623 PRELIMINARY;
077623;
01-NOV-1998 (TIEMBLrel. 08, C.
01-NOV-1998 (TIEMBLrel. 08, L.
01-MAR-2002 (TIEMBLrel. 20, L.
Caspase-3 (Fragment).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        PRINTS; PRO0376; ILIBCENZYME.
SMART; SM00115; CASC; 1.
PROSITE; PS01122; CASPASE_CYS; 1
PROSITE; PS01121; CASPASE_HIS; 1
PROSITE; PS0207; CASPASE_P10; 1
PROSITE; PS50208; CASPASE_P20; 1
PROSITE; PS50208; CASPASE_P20; 1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Ovis aries (Sheep).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Eutel
Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora;
Bovidae; Caprinae; Ovis.
                                                                                                                                                                                                                                                                                                                                                                                                                                                       Rueda B.R., Hendry I.R., Tilly J.L., Hamernik D.L.;
"Accumulation of Caspase-3 mRNA and Induction of Caspase Activity
the Ovine Corpus Luteum Following Prostaglandin-F2a Treatment In
                                                                                                                                                                                                                                                                                                                                                                                          Submitted (MAY-1998) to the EMBL/GenBank/DDBJ databases EMBL; AF068837; AAC25713.1; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                               Vivo."
                                                                                                                                                                                                                                                                                                                                              MEROPS; C14.003;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Pfam; PF00655; ICE_p10; Pfam; PF00656; ICE_p20;
                                                                                                                                                                                                                                                                                           InterPro; IPR002398; InterPro; IPR002138;
                                                                                                                                                                                                                                                                                                                                                                   HSSP; P42574;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            NCBI_TaxID=9940;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     245
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       180;
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Last annotation update)
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Pred. No. 2.9e
#3; Mismatches
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                 B5860C6996C21BE7 CRC64;
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.9e-72;
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Query Match

Score 854;

DВ

Length 182;

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RESULT 7
Q98UIB
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                                                                                                                                                                                                                                                                      Query Match
Best Local
                                                                                                                                                                                                                                                     Matches
                                                                                                                                                                                                                                                                                                                      Pfam; PF00655; ICE_P10; 1.

Pfam; PF00656; ICE_P20; 1.

Pfam; PF00656; ICE_P20; 1.

PRINTS; PR00376; ILIBCENZYME.

SMART; SM00115; CASC; 1.

PROSITE; PS01122; CASPASE_H15; UNKNOWN_1.

PROSITE; PS01121; CASPASE_H15; UNKNOWN_1.

PROSITE; PS0207; CASPASE_P10; 1.

PROSITE; PS50208; CASPASE_P20; 1.

SEQUENCE 282 AA; 31522 MW; 13C3454F5E099
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Q98UIB;
01-JUN-2001
01-JUN-2001
01-JUN-2002
                                                  , 157
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InterPro; IPR002138; ICE_p10.
InterPro; IPR001309; ICE_p20.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Mammallan Caspase 3.",
Submitted (AUG-2000) to the
EMBL; AB047003; BAB32409.1;
HSSP; P42574; 1PAU.
MEROPS; C14.003; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Brachydanio rerio (Zebrafish)
Eukaryota; Metazoa; Chordata;
Actinopterygii; Neopterygii; T
Cyprinidae; Danio.
NCBI_TaxID-7955;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Caspase-3
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             SEQUENCE FROM N.A.
Yabu T., Okazaki T.,
            160
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ZFIN; ZDB-GENE-011210-1;
                                                                                         100
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        "Molecular Cloning and Gene Expression
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            212
                                                                                                                                                                                                                                                                      Local Similarity
                                                                                                                             97
                                                                                                                                                                      40
                                                                                                                                                                                 37 YKMDYPEMGLCIIINNKNFHKSTGMTSRSGTDVDAANLRETFRNLKYEVRNKNDLTREEI 96
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LFIIQACRGTELDCGIETDSGVDDDM--ACHKIPVEADFLYAYSTAPGYYSWRNSKDGSW
                                                                           YSLNYPNIGHCIIINNKNFDRRTGMNPRNGTDVDAGNVMNVFRKLGYIVKVYNDQTVAQI
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l (TrEMBLrel.
2 (TrEMBLrel.
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                                                                                                                                                                                                                                                                53.5%;
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                                                                                                                                                                                                                                           Score 782; DB 13;
Pred. No. 1.5e-57;
32; Mismatches 58;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     EMBL/GenBank/DDBJ
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Last annotation update)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ) (Zebra danio).
; Craniata; Vertebrata; Euteleostomi;
Teleostei; Ostariophysi; Cypriniform
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Pred. No.
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                                                                                                                                                                                                                                                                                                       1.
13C3454F5E09932E CRC64;
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ches 11;
                                                                                                                                                                                                                                             58;
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                                                                                                                                                                                                                                                         Query Match
Best Local S
Matches 153
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                                                                                                                                                                                                                                                                                                                                                                            InterPro; IPR002398; ICE
InterPro; IPR002138; ICE
InterPro; IPR001309; ICE
Pfam; PF00655; ICE_D10;
Pfam; PF00655; ICE_D20;
                                                                                                                                                                                                                                                                                                  PROSITE; PSO1122; CASPASE_CYS; PROSITE; PSO1121; CASPASE_HIS; PROSITE; PSSO207; CASPASE_P20; PROSITE; PSSO208; CASPASE_P20; SEQUENCE 318 AA; 35937 MW;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   01-OCT-2000
01-OCT-2000
01-MAR-2002
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             SEQUENCE FROM N.A.
MEDLINE-20209426; PubMed=10744739;
Nakajima K., Takahashi A., Yaoita Y.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       XCASPASE-7.
Xenopus laevis (African clawed frog).
Chordata; Craniata;
                                                                                                                                                                                                                                                                                                                                                        PRINTS; PR00376; ILIBCENZYME SMART; SM00115; CASC; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                             J. Biol. Chem. 275:
EMBL; AB038170; BAA
HSSP; P42574; 1PAU.
                                                                                                                                                                                                                                                                                                                                                                                                                                    MEROPS; C14.004;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                            family.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Nakajima K., Takahashi A., Yaoita Y.
"Structure, expression and function
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            NCBI_TaxID=8355;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Amphibia; Batrachia; Xenopodinae; Xenopus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Caspase-7
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Q9IB65;
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                                         264
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                                    NEYGKELEVMQILTRVNFLVATQFESYSDDPQFSKKKQIPCVVSMLTKELYF
                                                 KQYADKLEFMHILTRVNRKVATEFESFSFDATFHAKKQIPCIVSMLTKELYF
                                                                              DGLEADSGSVNDSLETDANPRHKIPVEADFLYAYSTVPGYYSWRNPGMGSWFVQALCSVL
                                                                                           KRSSFVCVLLSHGEEGIIFGTNGPVDLKKITNFFRGDRCRSLTGKPKLFIIQACRGTELD
                                                                                                                                                                               INNKNFHKSTGMTSRSGTDVDAANLRETFRNLKYEVRNKNDLTREEIVELMRDVSKEDHS
                                                                                                                                                                                                             EEGEDSVDAKPDRSQRFSIFSSTKKKKVEDKPPKTNNNVRIVTPAFQYKMNNGNVGRCII
                                                                                                                                                                                                                                 ENTENSVDSKSIKNLEPKIIHGSESM---DSGISLDNS----YKMDYPEMGLCII 49
                                                                                                                          DSACFACIFLSHGEEGLIYGTDGAMPIKVLTTLFRGDNCRSLVGKPKLFFIQACRGHEFD
                                                                                                                                                                  INNKIFDKITGMGARNGTDIDARELLRCFKGLGFDVNVYNNKSCEEMENLLRTVAQQDHK 143
                                                                                                                                                                                                                                                            153;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     FIQSLCAMLKQYADKLEFMHILTRVNRKVATEFESFSFDATFHAKKQIPCIVSMLTKELY
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                                                                                                                                                                                                                                                                    Similarity
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                                                                                                                                                                                                                                                           Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                                                                                                                                               275:10484-10491(2000)
                                                                                                                                                                                                                                                                                                                                                                                                                                                        BAA94748.1;
                                                                                                                                                                                                                                                                    52.0%;
                                                                                                                                                                                                                                                                                                                                                                                                ICE_p10.
ICE_p20.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Anura; Mesobatrachia;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    15,
15,
20,
                                                                                                                                                                                                                                                                 Score 761; DB 1 Pred. No. 1e-55;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Last sequence up
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Created)
                                                                                                                                                                                                                                                                                                  6EBC6684AF86A128 CRC64;
                                                                                                                                                                                                                                                                                                                                  UNKNOWN_1.
                                                                                                                                                                                                                                                        Mismatches
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Vertebrata;
                                                                                                                                                                                                                                                                           DB 13;
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                                                                                                                                                                                                                                                        78;
                                                                                                                                                                                                                                                                           Length 318;
                                                                                                                                                                                                                                                        Indels
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Pipidae;
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Query Match
Best Local S
Matches 153
                                                            Mus musculus (Mouse).
Eukaryota; Metazoa; C
Mammalia; Eutheria; R
NCBI_TaxID=10090;
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InterPro; IPR002138; ICE_p10
InterPro; IPR0031309; ICE_p20
InterPro; IPR001309; ICE_p20
Pfam; PF00655; ICE_p10; 1.
Pfam; PF00656; ICE_p20; 1.
                                                                                                                                                                           01-JUN-2001
01-JUN-2001
01-MAR-2002
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        01-NOV-1998
01-NOV-1998
01-MAR-2002
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    PROSITE: PSO1122; CASPASE_CYS; PROSITE: PSO1121; CASPASE_HIS; PROSITE; PSSO207; CASPASE_P10; PROSITE: PSSO208; CASPASE_P20; SEQUENCE 303 AA; 34324 MW;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          "Rat caspase-7 sequence.";
Submitted (JUN-1998) to the EMBL/GenBank/DDBJ databases
EMBL; AF072124; AAC24011.1; -.
       Strausberg R.;
                           SEQUENCE FROM N.A.
                                                                                                                                                          Caspase 6.
                                                                                                                                                                                                                                      Q99M47;
                                                                                                                                                                                                                                                       Q99M47
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              PRINTS; PR00376; IL1BCENZYME. SMART; SM00115; CASc; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      TISSUE-SPLEEN;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; E
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Rattus norvegicus (Rat).
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          114
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                                                                                                                                                                                                                                                                                                                                                                                                                                         TDSGVDDDMAC---HKIPVEADFLYAYSTAPGYYSWRNSKDGSWEIQSLCAMLKQYADKL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 FVCVLLSHGEEGIIFGTNGPVDLKKITNFFRGDRCRSLTGKPKLFIIQACRGTELDCGIE 173
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        EIMQILTRVNDRVARHFESQSDDPRFNEKKQIPCMVSMLTKELYF 301
                                                                                                                                                                                                                                                                                                                                                                     EFMHILTRVNRKVATEFESFSFDATFHAKKQIPCIVSMLTKELYF 275
                                                                                                                                                                                                                                                                                                                                                                                                                   ADSGPINDTDANPRYKIPVEADFLFAYSTVPGYYSWRNPGKGSWFVQALCSILNEHGKDL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              STEDGVDAKPDRSTIISSLLWKKKKNASMCPVSTTRDRVPTYLYRMDFEKMGKCIIINNK
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     NTENSVDSKS-----IKNLEPKIIHGSESMDSGISLDN----SYKMDYPEMGLCIIINNK 53
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            P42574;
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8 (TrEMBLrel. 08,
2 (TrEMBLrel. 20,
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l (TrEMBLrel.
2 (TrEMBLrel.
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                                                                                                                                                                                                                                                     PRELIMINARY;
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                                                                                 Chordata;
Rodentia;
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53.7%;
                                                                                                                                                                           17,
17,
20,
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Last seq
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Last annotation updat
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Pred. No. 2.1e-54;
1; Mismatches 79;
                                                                                 Craniata; Vertebrata; Euteleostomi; Sciurognathi; Muridae; Murinae; Mus
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A71728754BF199DD CRC64;
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; Murinae; Rat
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              12;
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Best Local
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Q9BQE7;
Q1-JUN-2001 (TrEMBLrel. 17, Created)
O1-JUN-2001 (TrEMBLrel. 17, Last sequence update)
O1-JUN-2001 (TrEMBLrel. 21, Last annotation update)
O1-JUN-2002 (TrEMBLrel. 21, Last annotation update)
InterPro; IPR002398; ICE_p10.
InterPro; IPR002138; ICE_p10.
InterPro; IPR001309; ICE_p20.
InterPro; ICE_p10; I.
Pfam; PF00656; ICE_p20; 1.
                                                                                                               Submitted (NOV-2000) to the EMBL; BC004460; AAH04460.1; EMBL; BC000305; AAH00305.1; HSSP; P42574; 1PAU.
                                                                                                                                                                                         Strausberg R.;
                                                                                                                                                                                                            SEQUENCE FROM
TISSUE-LUNG;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Q9BQE7
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       PROSITE; PSO1122; CASPASE_CYS; PROSITE; PSO1121; CASPASE_HIS; PSO207; CASPASE_P10; PROSITE; PS50208; CASPASE_P20; SEQUENCE 276 AA; 31563 MW;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Pfam; PF00655; ICE_p10; 1.
Pfam; PF00656; ICE_p20; 1.
PRINTS; PR00376; IL1BCENZYME.
SMART; SM00115; CASC; 1.
                                                                                                                                                                                                                                                                   Submitted
                                                                                                                                                                                                                                                                                       Strausberg
                                                                                                                                                                                                                                                                                                        TISSUE-LUNG;
                                                                                                                                                                                                                                                                                                                          SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                Mammalia; Eutheria;
                                                                                                                                                                                                                                                                                                                                                                                                Eukaryota; Metazoa;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             InterPro; IPR002398; ICE.
InterPro; IPR002138; ICE_p10.
InterPro; IPR001309; ICE_p20.
                                                                                                 MEROPS;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           HSSP;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Submitted (JAN-2001) to the EMBL/GenBank/DDBJ databases
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  260
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         20
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                                                                                                 C14.005;
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                                                                                                                                                                                                                                                                   (MAR-2001)
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                                                                                                                                                                       EMBL/GenBank/DDBJ databases
                                                                                                                                                                                                                                                                   EMBL/GenBank/DDBJ databases
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Pred. No. 3.8e
42; Mismatches
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5965C5932A127B6C CRC64;
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8.8e-36;
nes 93;
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Best Local S
Matches 109
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Best Local S
Matches 105
                                                                                                                                                                                                                                                                                                                                                                    SEQUENCE FROM N.A.
Laing K.J., Holland J., Bonilla S., Cunni
"Cloning and sequencing of caspase 6 in 1
mykiss, and analysis of its expression ur
induce apoptosis.";
Submitted (DEC-1999) to the EMBL/GenBank,
EMBL; AF212219; AAF73848.1; -.
HSSP; P42574; 1PAU.
                                                                                                        Pfam; PF00655; ICE_D10; I.

Pfam; PF00656; ICE_D20; 1.

PRINTS; PR00376; ILIBCENZYME.

SMART; SM00111; CASCA; 1.

PROSITE; PS01122; CASCASE_HIS; I.

PROSITE; PS01121; CASCASE_HIS; I.

PROSITE; PS01121; CASCASE_P10; I.

PROSITE; PS0177; CASCASE_P10; I.

PROSITE; PS50208; CASCASE_P20; I.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Oncorhynchus mykiss (Rainbow trout) (Salmo gairdneri). Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleos Actinopterygii; Neopterygii; Teleostei; Euteleostei; Protacanthopterygii; Salmoniformes; Salmonidae; Oncorhynchus NCBI_TaxID-8022;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    01-OCT-2000 (TrEMBLrel.
01-OCT-2000 (TrEMBLrel.
01-MAR-2002 (TrEMBLrel.
Caspase 6.
                                                                                                                                                                                                                                                                            InterPro; IPR002398; ICE_P10
InterPro; IPR002138; ICE_P10
InterPro; IPR001309; ICE_P20
Bfm: PEOCEFE TENTO ICE_P20
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SMART; SM
PROSITE;
PROSITE;
PROSITE;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            37
    109;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         CIVSMLTKELYFY 276
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       YSWRNSKDGSWFIQSLCAMLKQYADKLEFMHILTRVNRKVATEFESFSFDATFHAKKQIP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          YSHRETVNGSWYIQDLCEMLGKYGSSLEFTELLTLVNRKVSQRRVDFCKDPSAIGKKQVP
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        VELMRDVSKEDHSKRSSFVCVLLSHGEEGIIFGTNGPVDLKKITNFFRGDRCRSLTGKPK
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PS01121; CASPASE_HIS;
PS50207; CASPASE_P10;
PS50208; CASPASE_P20;
                                                                                              302
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                293 AA;
        Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         PRELIMINARY;
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                                                                                           AA;
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                                                                                           34082 MW;
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Last sequence update)
Last annotation updat
                                                                                                                                                                                                                                                                                                                                                                                            EMBL/GenBank/DDBJ
Score 525.5; DB 13;
Pred. No. 4.7e-36;
3; Mismatches 97;
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Pred.
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No. 4.
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                                         DB 13;
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      Indels
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s known to
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    27;
  Gaps
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Matches 109
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HSSP; P42574; ICE
MEROPS; C14.005;
                                                                                                                                                                                                                                                                                                                                                                                            PROSITE; PSO1122; CASPASE_CYS; PROSITE; PSO1121; CASPASE_PIO; PROSITE; PSO50207; CASPASE_P20; PROSITE; PSSO208; CASPASE_P20; SEQUENCE 303 AA; 34132 MW;
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01-OCT-2000 (TrEMBLrel.
01-OCT-2000 (TrEMBLrel.
01-MAR-2002 (TrEMBLrel.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          PRINTS; PR00376; ILIBCENZYME. SMART; SM00115; CASc; 1.
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InterPro; IPR002138; ICE_p10.
InterPro; IPR001309; ICE_p20.
Pfam; PF00655; ICE_p10; 1.
Pfam; PF00656; ICE_p20; 1.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Amphibia; Batrachia; Anura; Mesobatrachia; Pipoidea; Pipidae; Xenopodinae; Xenopus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              SEQUENCE FROM N.A. MEDLINE-20209426; PubMed=10744739; Nakajima K., Takahashi A., Yaoita
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             J. Biol.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Caspase-6
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Q9IB66
Xenopus laevis (African clawed frog).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         242 CGAMRKFGDSLEFTELLTLVNRKVSMRSVGNCNDKTAIGKKOVPCFASMLTRKLYF
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                                                                                                                                                                                                            182
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                                                                                                                         NDLTREEIVELMRDVSKEDHSKRSSFVCVLLSHGEEGIIFGTNGPVDLKKITNFFRGDRC
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                                                                              YNLRTMDVLEKIQEASTTDHSNADCFLCVFLSHGEDKHIYSYDSLIDIQELTNPFKGDKC
                                                                                                                                                                               VELDPSAEYIMTHKRRGLALIFNHEDFYWQLRLGSRRGTNTDSMNLNRILTDLGFDVQNY 101
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             -----LDCGIETDSGVDDDMACHKIPVEADFLYAYSTAPGYYSWRNSKDGSWFIQSL
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                                                                                                                                                                                                                                                                                                                      Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Chem. 275:10484-10491(2000).
038169; BAA94747.1; -.
                                                                                                                                                                                                                                                                                           Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       1CP3
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                                                                                                                                                                                                                                                                                                                   42.48;
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15,
20,
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, Last sequence up
, Last annotation
                                                                                                                                                                                                                                                                                        Score 524; DB 13;
Pred. No. 6.3e-36;
8; Mismatches 86
                                                                                                                                                                                                                                                                                                                                                                                            4C54A0A607C69756 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                303
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                                                                                                                                                                                                                                                                                     Indels
                                                                                                                                                                                                                                                                                        14;
                                                                                                                                                                                                                                                                                   Gaps
                                                                                                                              148
                                                                                                                                                                                                                                     88
                                                                              161
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RESULT 14
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RA Arakawa T., Hara A., Fukunishi Y., Konno H., Adachi J., Fukuda S.,
RA Alzawa K., Izawa M., Nishi K., Kiyosawa H., Kondo S., Yamanaka I.,
RA Alzawa K., Izawa M., Nishi K., Kiyosawa H., Kondo S., Yamanaka I.,
RA Kadota K., Matsuda H.A., Ashburner M., Batalov S., Casavant T.,
RA Kadota K., Matsuda H.A., Ashburner M., Batalov S., Casavant T.,
RA Kuchl P., Lewis S., Matsuo Y., Nikaido I., Pesole G., Quackenbush J.,
RA Kuchl P., Lewis S., Matsuo Y., Nikaido I., Pesole G., Quackenbush J.,
RA Kuchl P., Lewis S., Matsuo Y., Nikaido I., Pesole G., Quackenbush J.,
RA Kuchl P., Lewis S., Matsuo Y., Nikaido I., Pesole G., Quackenbush J.,
RA Kuchl P., Lewis S., Matsuo Y., Nikaido I., Pesole G., Quackenbush J.,
RA Schriml L.M., Staubil F., Suzuki R., Tomita M., Wagner L., Washio T.,
RA Schai K., Okido T., Frunno M., Aono H., Baldarcelli R., Barsh G.,
RA Sakai K., Okido T., Frunno M., Aono H., Baldarcelli R., Barsh G.,
RA Blake J., Boffelli D., Bojunga N., Carninci P., de Bonaldo M.F.,
RA Blake J., Boffelli D., Hofmann M., Hume D.A., Kamiya M., Lee N.H.,
RA Blake J., Marchionni L., Mashima J., Mazzarelli J., Mombaerts P.,
RA Burons P., Marchionni L., Mashima J., Mazzarelli J., Mombaerts P.,
RA Nordone P., Ring B., Ringwald M., Rodriguez I., Sakamoto N.,
Ra Sasaki H., Toyo-oka K., Wang K.H., Weltz C., Whittaker C., Wilming L.,
RA Hayashiraki V., Yoshida K., Hasegawa Y., Kawaji H., Kohtsuki S.,
                                                         Matches
                                                                                     Query Match
                                                                                                                                PROSITE;
PROSITE;
PROSITE;
PROSITE;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   SEQUENCE FROM N.A.
STRAIN=C57BL/6J; TISSUE-EMBRYO;
MEDLINE-21085660; PubMed-11217851;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    01-JUN-2001 (TREMBLrel. 17, Created)
01-JUN-2001 (TREMBLrel. 17, Last sequence update)
01-JUN-2002 (TREMBLrel. 21, Last annotation update)
10 days embryo cDNA, RIKEN full-length enriched library,
clone:2610037G10, full insert sequence.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Q9D089;
01-JUN-2001
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Q9D089
                                                                                                                                                                                                               InterPro; IPR002198; ICE_p10.
InterPro; IPR002138; ICE_p10.
InterPro; IPR00109; ICE_p20.
Pfam; PF00655; ICE_p10; 1.
Pfam; PF00656; ICE_p20; 1.
                                                                                                                                                                                                                                                                                                     Nature 409:685-690(2001).
EMBL; AK011710; BAB27792.1; -.
HSSP; P42574; 1PAU.
                                                                                                                                                                                      PRINTS; PR00376; ILIBO SMART; SM00115; CASC;
                                                                                                                                                                                                                                                                                           MGD; MGI:1312921;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Mus musculus (Mouse).
Eukaryota; Metazoa; Chordata;
Mammalia; Eutheria; Rodentia;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          CASP6
                                                                                                                                                                                                                                                                                                                                                                Hayashizaki Y.;
                                                                                                                                                                                                                                                                                                                                           Functional annotation of a full-length mouse cDNA collection."
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                281 GKKQIPCFASMLTKKLF 297
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            258
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        221
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                               37
  20
                       YKMDYPEMGLCIIINNKNFHKSTGMTSRSGTDVDAANLRETFRNLKYEVRNKNDLTREEI 96
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    STAPGYYSWRNSKDGSWFIQSLCAMLKQYADKLEFMHILTRVNRKVATEFESFSFDATFH 257
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             AKKQIPCIVSMLTKELY 274
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     SVAEGYYSHRETVNGSWYIQDLCAVVKAYAASLEFTEILTLVNRKVSQRSVEYCNDPKAI 280
YKMDHKRRGVALIFNHERFFWHLTLPERRGTNADRDNLTRRFSDLGFEVKCFNDLRAEEL 79
                                                                                                               2; PS01122; CASPASE_CYS; 1

3; PS01121; CASPASE_HIS; 1

3; PS50207; CASPASE_P10; 1

3; PS50208; CASPASE_P20; 1

3; PS50208; CASPASE_P20; 1

3; PS50208; CASPASE_P20; 1
                                                                        Similarity
                                                           Conservative
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                                                                                                                                                                                                     ILIBCENZYME
                                                                                                                                                                                                                                                                                        Casp6
                                                                     35.3%;
                                                      42;
                                                        Score 516; DB Pred. No. 2.6e
                                                                                                            ; 1.
1.
; 1.
; 1.
597EDF2321126B6C CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Craniata; Vertebrata; Euteleostomi; Sciurognathi; Muridae; Murinae; Mus
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         276
                                                      DB 11;
2.6e-35;
les 94;
                                                                                     DB
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                                                                                  Length 276;
                                                        Indels
                                                        12;
                                                      Gaps
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                                                                                                                                         Query Match
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01-NOV-1998
01-JUN-2002
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                                                                                                                                                                                                                                                                                                                              MEROPS; C14.005
                                                                                                                                                                                                                                                                                                                                             HSSP; P42574;
                                                                                                                                                                                                                                                                                                                                                                                                                                                            PubMed=11953316
                                                                                                                                                                                                                                                                                                                                                                                                                                                                         SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      NCBI_TaxID=9031;
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                                                                                                                            Loca:
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Pfam; PF00655; ICE_P10; 1.
Pfam; PF00656; ICE_P20; 1.
PRINTS; PR00376; IL1BECENZYME.
SMART; SM00115; CASC; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           "Caspase-6 gene disruption reveals a requirement for lamin A cleavage in apptotic chromatin condensation."; EMBO J. 21:1967-1977(2002).
EMBL; AF082329; AAC32378.1; -.
EMBL; AF469049; AAL82386.1; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    SEQUENCE FROM N.A.
MEDLINE-20149872; PubMed-10684799;
Johnson A.L., Bridgham J.T.;
"Caspase-3 and -6 expression and enzyme
                                                                                                                                                                                                                                                           PROSITE; PS0112; CASPASE_CYS;
PROSITE; PS50207; CASPASE_P10;
PROSITE; PS50208; CASPASE_P20;
SEQUENCE 304 AA; 34534 MW;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Gallus gallus (Chicken).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Biol. Reprod. 62:589-598(2000).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Ruchaud S., Korfali N., Villa P., Kottke T.J., Dingwall
Kaufmann S.H., Earnshaw W.C.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Eukaryota; Metazoa; Chordata; (
Archosauria; Aves; Neognathae;
                                                                                                                                                                                                                                                                                                                                                                                                                                    InterPro; IPR002138;
InterPro; IPR001309;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                               interPro; IPR002398;
109 LKKVFEASRDDYSNADCFVCVFLSHGENDHVYAYDAQIKIETITNMFRGDKCQSLVGKPK 168
                                                                                                                            37 YKMDYPEMGLCIIINNKNFHKSTGMTSRSGTDVDAANLRETFRNLKYEVRNKNDLTREEI 96
                                        VELMRDVSKEDHSKRSSFVCVLLSHGEEGIIFGTNGPVDLKKITNFFRGDRCRSLTGKPK 156
                                                                                    YKMNHQRRGVALIFNHEHFFWHLRLPDRRGTLADRNNLKRSLTDLGFEVRIFDDLKAEDV 108
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           SHRETVNGSWYIQDLCEMLARYGSSLEFTELLTLVNRKVSQRRVDFCKDPDAIGKKQVPV
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      SWRNSKDGSWFIQSLCAMLKQYADKLEFMHILTRVNRKVATEFESFSFDATFHAKKQIPC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                IFIIQACRGSQHDVPVVPLDMVDHQTDKLDNVTQVDAASVYTLPAGADFLMCYSVAEGYY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        LFIIQACRGTELDCGIETDSGVD-----
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                                                                                                                                                                      102; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            (TrEMBLrel. 08, (TrEMBLrel. 08, (TrEMBLrel. 21,
                                                                                                                                                                      Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  PRELIMINARY;
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                                                                                                                                                                                                                                                                                                                                                                                                                                  ICE_p10.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Chordata; Craniata; Vertebrata; Euteleostomi;
Neognathae; Galliformes; Phasianidae; Phasiani
                                                                                                                                                                                        35.2%;
40.5%;
                                                                                                                                                                      46;
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51CE31EBCAAE7383 CRC64;
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Db Db Db Searc	Qy
Db 169 IFIIQACROKHDDPVLVQDSVDSKDETTVNQTEVDAAGVYTLPAGADFIKCYSVAQGYF 228 Qy 205 SWRNSKDGSWFIQSLCAMLKQYADKLEFMHILTRVNRKVATEFESFSFDATFHAKKQIPC 264 : : : : : :	157 LFIIOACRGTEIDCGTETDGGVDDDMACHKIDWDADGTVAVGMADGWV 201

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Result
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Maximum Match 100%
Listing first 45 summaries
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Total number of hits satisfying chosen parameters:
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.
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3: pir3:*
4: pir4:*
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Copyright (c) 1993 - 2002 Compuq
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ); Search time 15.2828 Seconds (without alignments) 1742.436 Million cell updates/sec
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                                                  caspase protein 3
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caspase protein 1C
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45	44	43	42	41	40	39	38	37	36	35	34	33	32	31	30
87.5	87.5	87.5	87.5	88	88	88	88	68	90.5	91	91.5	92.5	93	96	100.5
6.0	6.0	6.0	6.0	6.0	6.0	6.0	6.0	6.1	6.2	6.2	6.3	6.3	6.4	6.6	6.9
556	554	552	299	1087	781	600	537	2052	534	629	642	5255	534	537	457
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806838	G01928	S17551	D81384	T30330	C69452	S28496	TVHUSY	C97038	A44991	AE2497	D88951	T31677	S33568	I51592	T05439
gamma-aminobutyric	gamma-aminobutyric	gamma-aminobutyric	probable lipoprote	gelsolin-related p	signal-transducing	microtubule-associ	protein-tyrosine k	phage-related prot	protein-tyrosine k	hypothetical prote	protein C38C3.7 [i	bacitracin synthet	protein-tyrosine k	protein-tyrosine k	hypothetical prote

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A;Residues: 1-189,'E',191-277 <RES>
A;Cross references: EMBL:U26943; NID:g857568; PIDN:AAA74929.1; PID:g857569
C;Keywords: apoptosis; cysteine proteinase; hydrolase; lymphocyte
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          A;Molecule type: protein
A;Residues: 29-46;176-189,'E',191-193 <NIC>
R;Tewari, M.; Quan, L.T.; O'Rourke, K.; Desnoyers, S.; Zeng, Z.; Beidler, D.R.; Poiri Cell 81, 801-809, 1995
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         A;Cross-references: GB:U13737; NID:g561665; PIDN:AAA65015.1; PID:g561666 R;NiCholson, D.W.; All, A.; Thornberry, N.A.; Vaillancourt, J.P.; Ding, C.K.; Gallant; Yu, V.L.; Miller, D.K.
Nature 376, 37-43, 1995
A;Title: Identification and inhibition of the ICE/CED-3 protease necessary for mammal A;Reference number: S58899; MUID:95319529; PMID:7596430
A;Accession: S58899
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         cysteine proteinase (EC 3.4.22.-) CPP32 precursor - human
(Alternate names: cysteine proteinase CPP32
C;Species: Homo sapiens (man)
C;Date: 06-Feb-1995 #sequence_revision 06-Feb-1995 #text_change 01-Dec-2000
C;Accession: A55315; S58899; I39005
R;Fernandes-Alnemri, T; Litwack, G; Alnemri, E.S.
J. Biol. Chem. 269, 30761-30764, 1994
A;Title: CPP32, a novel human apoptotic protein with homology to Caenorhabditis elega
A;Reference number: A55315; MUID:95074098; PMID:7983002
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             A;Title: Yama/CPP32 beta, a mammalian homolog of CED-3, is a CrmA-inhibitable proteas A;Reference number: A56924; MUID:95292347; PMID:7774019 .
A;Accession: I39005
A;Status: preliminary
A;Molecula tune. mBNA
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A;Molecule type: mRNA
A;Residues: 1-277 <FER>
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Best Local S
Matches 276
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DMACHKIPVEADFLYAYSTAPGYYSWRNSKDGSWFIQSLCAMLKQYADKLEFMHILTRVN
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                                                                                      HGEEGIIFGTNGPVDLKKITNFFRGDRCRSLTGKPKLFIIQACRGTELDCGIETDSGVDD 180
                                                       {\tt HGEEGIIFGTNGPVDLKKITNFFRGDRCRSLTGKPKLFIIQACRGTELDCGIETDSGVDD}
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99.6%; Pred. No. 2.1e-111;
Live 1; Mismatches 0;
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RESULT 2
S064710
Cysteine proteinase (EC 3.4.22.-) CPP32 - Chinese hamster
C;Species: Cricetulus griseus (Chinese hamster)
C;Date: 14-Feb-1997 #sequence_revision 13-Mar-1997 #text_change 05-Nov-1999
C;Date: 14-Feb-1997 #sequence not 3-Mar-1997 #text_change 05-Nov-1999
C;Date: 14-Feb-1997 #sequence not shair in the company of sterol regulatory element binding proteins (SREBPs) by CPP32
A;Reference number: S64710; MUID:96183185; pMID:8605870
A;Accession: S64710
A;Accession: S64710
A;Accession: S72395
A;Molecule type: mRNA
A;Reference number: S72395
A;Molecule type: mRNA
A;Residues: 1-79; A;81-146; Y',148-277 <WAW>
A;Cross-references: EMBL:027463; NID:91244443; PIDN:AAB01511.1; PID:g1244444
C;Keywords: apoptosis; cysteine proteinase; hydrolase
                                                                                                                                                                                                                                                           RESULT
JC5410
A;Status: nucleic acid sequence
A;Molecule type: mRNA
A;Residues: 1-277 <MUK>
A;Experimental source: embryo
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C:Species: Mus musculus (house mouse)
C:Date: 10-Jun-1997 #sequence_revision 18-Jul-1997 #text_change
C:Accession: JC5410
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                                                                                       Blochem Biophys. Res. Commun. 231, 770-77. A;Title: Specific expression of CPP32 in st A;Reference number: JC5410; MUID:97224429; A;Accession: JC5410
                                                                                                                                               R;Mukasa, T.; Urase, K.; Momoi, M.Y.; Kimura, T.; Biochem. Biophys. Res. Commun. 231, 770-774, 1997
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caspase-9 long chain - mouse
C;Species: Mus musculus (house mouse)
C;Date: 23-Mar-2001 #sequence_revision
C;Accession: JC7123
R;Fujita, E.; Jinbo, A.; Matuzaki, H.;
                                                             RESULT
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A:Reference number: 153300, MUID:96042508; PMID:758824
A:Accession: 167437
A:Status: preliminary; translated from GB/EMBL/DDBJ
A:Molecule type: mRNA
A:Residues: 1-212 <RES>
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C;Species: Rattus norvegicus (Norway rat)
C;Date: 26-Jul-1996 #sequence_revision 26-Jul-1996 #te
C;Accession: 167437
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167437
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87.7%;
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Pred. No. 8.
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Pred. No. 8.2e-98;
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protein

similar to mammalian

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C:Species: Homo sapiens (man)
C:Date: 21-Dec-1996 #sequence_revision 06-Jun-1997 #text_change 05-Nov-1999
C:Accession: G02635
R;Duan, H.; Orth, K.; Chinnaiyan, A.M.; Poirier, G.G.; Froelich, C.J.; He, V submitted to the EMBL Data Library, April 1996
A;Reference number: H01513
A;Accession: G02635
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A;Cross-references: EMBL:U56390; NID:g1336026; PIDN:AAC50640.1; PID:g1336027
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A; Residues: 1-416 < DUA>
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A;Residues: 1-454 <FUJ>
A;Cross-references: DDBJ:AB019600; NID:g6440941; PID:g6440942
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Biochem. Biophys. Res. Commun. 264, 550-555, 1999
A;Title: Akt phosphorylation site found in human caspase-9 is absent in mouse caspase-9
A;Reference number: JC7123; MUID:20001956; PMID:10529400
A;Accession: JC7123
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               A; Status: preliminary
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Best Local
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                                                                                                                                                                                                                                                                                                                                                                               DNSYKMDYPEMGLCIIINNKNFHKSTGMTSRSGTDVDAANLRETFRNLKYEVRNKNDLTR 93
                             AVSVK - -
                                                                                                                                                                                                                                                                          KKMVLALLELARQDHGALDCCVVVILSHGCQASHLQFPGAVYGTDGCPVSVEKIVNIFNG
                                                                                                                                                                                                                                                                                                                                                      DLAYILSMEPCGHCLIINNVNFCRESGLRTRTGSNIDCEKLRRRFSSLHFMVEVKGDLTA 209
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        AVSEK-----GTY---KQIPGCFNFLRKKLFF
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                                                                                                                                                                                                                       DRCRSLTGKPKLFIIQACRGTELDCGIETDSGVDDDM-----
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                                                               KVATEFESFSFDATFHAKKQIPCIVSMLTKELYF
                                                                                                                                                                                            TSCPSLGGKPKLFFIQACGGEQKDHGFEVASTSPEDESPGSNPEPDATPFQEGLRTFDQL 329
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              KVATEFESFSFDATFHAKKQIPCIVSMLTKELYF
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     SGCPSLGGKPKLFFIQACGGEQKDHGFEVACTSSQGRTLDSDSEPDATPFQEGPRPLDQL 367
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              EEIVELMRDVSKEDHSKRSSFVCVLLSHGEE------GIIFGTNG-PVDLKKITNFFRG 145
                                                                                                         DAISSLPTPSDIFVSYSTFPGFVSWRDPKSGSWYVETLDDIFEQWAHSEDLQSLLLRVAN
                                                                                                                                                                                                                                                                                                                  EEIVELMRDVSKEDHSKRSSFVCVLLSHGEE------GIIFGTNG-PVDLKKITNFFRG 145
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         -ACHKIPVEADFLYAYSTAPGYYSWRNSKDGSWFIQSLCAMLKQYADKLEFMHILTRVNR 241
                                                                                                                                                                                                                                                                                                                                                                                                                                                         Similarity
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                         -GIYKQMPGCFNFLRKKLFF
                                                                                                                                                                                                                                                                                                                                                                                                                                         28.6%; Score 418; DB 2; 33.2%; Pred. No. 2.2e-26; tive 51; Mismatches 90;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         29.9%; Score 437; DB 2 36.1%; Pred. No. 7e-28;
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R; Yuan, J.; Shaham, Cell 75, 641-652, 199
A; Title: The C. elega
                                                                                                                                                                                                                           hypothetical protein C48D1.2 - Caenorhabditis elegans C;Species: Caenorhabditis elegans C;Date: 15-Oct-1999 #sequence_revision 15-Oct-1999 #t/C;Accession: T20038 R;Burton, J.
                                                                                                                                                                                                                                                                                                                                   RESULT
T20038
A;Experimental source: clone C48D1
C;Genetics:
A;Gene: CESP:C48D1.2
A;Map position: 4
                                                                                                       A;Status: preliminary; translated A;Molecule type: DNA B;Residues: 1-495 <WIL>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             A;Title: The C. elegans cell death gene ced-3 encodes a A;Reference number: A49429; MUID:94061982; PMID:8242740 A;Accession: A49429
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                interleukin-1 beta-converting enzyme homolog CED-3 - Caenorhabditis elegans
C;Specles: Caenorhabditis elegans
C;Date: 07-Apr-1994 #sequence_revision 18-Nov-1994 #text_change 01-Dec-2000
C;Accession: A49429; T37312
R;Yuan, J; Shaham, S; Ledoux, S.; Ellis, H.M.; Horvitz, H.R.
                                                                                                                                                                       A; Reference number: A; Accession: T20038
                                                                                                                                                                                     submitted to the EMBL Data Library, October 1996 A; Reference number: Z19214
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                                                                                  A; Cross-references:
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A; Residues: 1-503 < YUA>
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                                                                                                                                                                                                                                                                                                                                                                                                                     YFW 495
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          GEEGIIFGTNG-PVDLKKITNFFRGDRCRSLTGKPKLFIIQACRGTELDCGIETDSGVD- 179
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         TSRSGTDVDAANLRETFRNLKYEVRNKNDLTREEIVELMRDVSKEDHSKRSSFVCVLLSH 121
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    WFIQAVCEVFSTHAKDMDVVELLTEVNKKVACGFQT---SQGSNILKQMPEMTSRLLKKF
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      WFIOSLCAMLKQYADKLEFMHILTRVNRKVATEFESFSFDATFHAKKQIPCIVSMLTKEL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    VPAFLRRGWDNRDGPLFNFLGCVRPQVQQVWRKKPSQADILIAYATTAQYVSWRNSARGS
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                                                                                                                                                                                                                                                                                                                                                                                                                                                              YFY 276
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                                                                                EMBL: Z81049; PIDN: CAB02848.1; GSPDB: GN00022; CESP: C48D1
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                                                                                                                                               GB/EMBL/DDBJ
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#text_change 15-Oct-1999

DB 2; 108;

Indels Length 503;

49;

Gaps

8

315

256 61

375

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RESULT 10
JC6507
caspase-2 - rat
C;Species: Rattus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        apoptosis regulator ICH-1, stimulatory form L - human C;Speciles: Homo sapiens (man) C;Date: 28-Apr-1995 #sequence_revision 28-Apr-1995 #text_change 17-Mar-1999 C;Accession: A54821 R;Wang, L.; Miura, M.; Bergeron, L.; Zhu, H.; Yuan, J. Cell 78, 739-750, 1994
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A;Residues: 1-435 <WAN>
A;Cross-references: GB:Ul3021; NID:g537291;
C;Keywords: alternative splicing; apoptosis
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                                                                                                                                                                                                                          IVALLSHGVEGAIYGVDGKLLQLQEVFQLFDNANCPSLQNKPKMFFIQACRGDETDRGVD
                                                                                                 LAQVFSERACDMHVADMLVKVNALI-KDREGYAPGTEFHRCKEMSEYCSTLCRHLYLF
                                                                                                                               LCAMLKQYADKLEFMHILTRVNRKVATEFESFSFDATFHAKKQIPCIVSMLTKELYFY
                                                                                                                                                              QQDGKNHAGSPGCEESDAG-KEKLPKMRLPTRSDMTCGYACLKGTAAMRNTKRGSWYIEA
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                                                                                                                                                                                                                                                                                       TGEKELEFRSGGDVDHSTLYTLFKLLGYDVHVLCDQTAQEMQEKLQNFAQLPAHRVTDSC
                                                                                                                                                                                                                                                                                                                    HKSTGMTSRSGTDVDAANLRETFRNLKYEVRNKNDLTREEIVELMRDVSK-EDHSKRSSF 114
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        norvegicus
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                                                                                                                                                                                 -ETDSGVDDDMACHKIPVEADFLYAYSTAPGYYSWRNSKDGSWFIQS 218
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32.18;
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        (Norway
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Pred. No. 4.5e-19;
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Pred. No. 6.4e-21;
        rat)
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C; Keywords: cy:
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A; Residues: 269-536 <
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A; Residues: 1-536 <SHA>
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A;Status: preliminary; translated from GB/EMBL/DDBJ
                                                                                                                                                                                                                                                                                                                                                                                          J. Biol. Chem. 273, 35109-35117, 1998
A; Title: Identification of multiple Caenorhabditis elegans
A; Reference number: Z22587; MUID:99074291; PMID:9857046
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C;Accession: T43633; T43636
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A;Title: Cloning and expression of the cDNA A;Reference number: JC6507; MUID:98087427; 1A;A;Accession: JC6507
                                                                                                                                                                 A; Map position:
                                                                                                                                                                                  A;Gene: csp-1
                                                                                                                                                                                                    C; Genetics:
                                                                                                                                                                                                                     A; Cross-references:
                                                                                                                                                                                                                                                                      A; Status: preliminary; translated
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A; Residues: 1-452 <SAT>
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YKMDYPEMGLCIIINNKNFHKSTGMTSRSGTDVDAANLRETFRNLKYEVRNKNDLTREEI 96
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                                    Score 310.5; DB 2;
Pred. No. 1.7e-17;
2; Mismatches 91;
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                                                                                                                                                                                                               NID:g4063369; PIDN:AAC98293.1;
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PMID:9427555
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T27021
hypothetical protein Y48E1B.13 - Caenorhabditis elegans C;Species: Caenorhabditis elegans
C;Date: 15-Oct-1999 #sequence_revision 15-Oct-1999 #tex
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C:Species: Caenorhabditis elegans
C:Date: 21-Jan-2000 #sequence_revision 21-Jan-2000 #text_change 21-Jul-2000
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A;Residues: 564-826 <
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              A; Molecule type: mRNA
A; Residues: 1-826 <SHA>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 A; Title: Identification of multiple Caenorhabditis elegans A; Reference number: Z22587; MUID:99074291; PMID:9857046 A; Accession: T43638
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              A;Status: preliminary; translated from GB/EMBL/DDBJ
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        C; Accession: T43638; T43639
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         caspase-related proteinase 2A (EC 3.4.22.-) - Caenorhabditis elegans
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                                                                                                                               KYEA-
                                                                                                                                                            EFESFSFDATFHAKKQIPCIVSMLTKELYF 275
                                                                                                                                                                                           TSSSQADLLVSFSTSPGFLSFRDETKGTWYIQELYRVIIENAKDTHLADLLMETNRRVVE 797
                                                                                                                                                                                                                            ---VEADFLYAYSTAPGYYSWRNSKDGSWFIQSLCAMLKQYADKLEFMHILTRVNRKVAT 245
                                                                                                                                                                                                                                                                                                                                                                  YEVRNKNDLTREEIVELMRDVSKEDHSKRSSFVCVLLSHGEEGIIFGTNG-PVDLKKITN 141
                                                                                                                                                                                                                                                                                                                                                                                                                                    ESMDSGISLDNSYKMDYPEMGLC--IIINNKNFHKSTGMTSRSGTDVDAANLRETFRNLK 82
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 AKKQIPCIVSMLTKELYF 275
                                                                                                                                                                                                                                                                                                 FFRGDRC-RSLTGKPKLFIIQACRGTELDCGIETDSGVDD------DMACHKIP---
                                                                                                                                                                                                                                                                                                                                                                                                     EDASDGKKIDETRKYRNNRSSKCRAIIINNVVF---CGMEKRIGSDKDKKKLSKLFERLG
                                                                                                                                                                                                                                                                                                                                   YQSTSYDNLKSSEILETVRQFTQSNHG--DSLIITIMSHGDQGLLYGVDGVPVQMLDIID
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   --KQAPEILSRLTKQWHF
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   STAPGYYSWRNSKDGSWFIQSLCAMLKQYADKLEFMHILTRVNRKVATEFESFSFDATFH
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           LEAIKEFAEMAHT--DSIILFLLSHGDGAGSVFGIDDMPVNVMEVSTYLAYH--QNLLLK
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Similarity
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                                                                                                                                                                                                                                                              -CTASLAKKPKWLMCVCCRGDRIDRAVRCDGFIDNFFDRFPKFFQFMKSKFPSHQ
                                                                                                                           -DKVVIVCKQAPEFWSRFTKQLFF
                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Score 306.5; DB 2
Pred. No. 6.2e-17;
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15-Oct-1999 #text_change
                                                                                                                           824
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 15-Oct-1999
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A; Introns: 9/3; 59/3; 135/1;
C; Keywords: differentiation
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A;Title: Caspase-14: Analysis of gene structure and mRNA expression
A;Reference number: JC7517; MUID:20517231; PMID:11062009
                                                                                                                                                                                                                                                                                                                                                                            C; Comment:
C; Genetics:
                                                                                                                                                                                                                                                                                                                                                                                                                                A; Molecule type: mRNA
A; Residues: 1-242 <ECK>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  C; Species: Homo sapiens (man)
C; Date: 30-Jun-2001 #sequence
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JC7517
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A; Accession: T27021
                                                                                                                                                                                                                                                                                                                                                          A;Gene: casp-14/a
                                                                                                                                                                                                                                                                                                                                                                                                              A; Cross-references: GB: AF097874
                                                                                                                                                                                                                                                                                                                                                                                                                                                                      A; Accession:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      A; Contents: Epidermal keratinocytes
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             R; Eckhart,
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A; Introns: 79/3; 122/3; 239/2; 286/3; 333/1; 417/3;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         C; Accession:
R; McMurray,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  A; Gene: CESP:Y48E1B.13
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    A;Cross-references: EMBL:Z93393; PII
A;Experimental source: clone Y48E1B
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         A; Molecule type: DNA
A; Residues: 1-642 <WIL>
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                                                                                                                                                                                                                                              Best
                                                                                                                                                                                                                                                                                                                                                                                         Comment: This enzyme accumulates during keratinocyte differentiation
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     117
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                       CRSLTGKPKLFIIQACRGTELDCGIETDSGVDDDMAC----HKIPVEADFLYAYSTAPGY 203
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       VELMRDVSKEDHSKRSSFVCVLLSHGE-EGIIFGTNG-PVDLKKITNFFRGDRCRSLTGK 154
CQALRAKPKVYIIQACRGEQRDPG-ETVGGDEIVMVIKDSPQTIPTYTDALHVYSTVEGY 175
                                                                                                                                                                                 DNSYKMDYPEMGLCIIINNKNFHKSTGMTSRSGTDVDAANLRETFRNLKYEVRNKNDLTR 93
                                                                       EQFQEELEKFQQAIDSREDPVSCAFVVLMAHGREGFLKGEDG - - EMVKLENLFEALNNKN 116
                                                                                                         EBIVELMRDVSKEDHSKRSSFVC --- VLLSHGEEGIIFGTNGPVDLKKITNFF --- RGDR 147
                                                                                                                                              EEKYDMSGARLALILCVTK------AREGSEEDLDALEHMFRQLRFESTMKRDPTA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    NSKDGSWFIQSLCAMLKQYADKLEFMHILTRVNRKVATEFESFSFDATFHAKKQIP
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 LEAIKEFAEMAHT -- DSIILFLLSHGDGAGSVFGIDDMPVNVMEVSTYLAYH -- QNLLLK 475
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            PKWVAVSACRGGEIDLIFFAFQPGTFTS---
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               L.; Ban,
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                                                                                                                                                                                                                                           18.8%;
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                                                                                                                                                                                                                                                                                                                  174/1;
                                                                                                                                                                                                                     39;
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                                                                                                                                                                                                                       Score 274.5; DB 2
Pred. No. 5.3e-15;
9; Mismatches 103
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Score 277; DB 2;
Pred. No. 1.1e-14;
                                                                                                                                                                                                                                                                                                                    208/3
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                                                                                                                                                                                                                                                          DB 2;
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Db 1/6 INVENDENCES PORTINDWERNREGHILERL/TEVERNAM-EMBLYOVBOKARKTNEP 229 Dy 230 ELOSTLERELY 240 RESULT 15 A46495 A46495 A46495 A11-1 beta convertase - mouses Ciphecis Num socilus (house mouse) A;Title: Molecular 120, 199, 1993 A;Title: Molecular 120, 199, 1993 A;Title: Molecular 120, 199, 1993 A;Title: Molecular 120, 1993 A;Title: The structure and compared with conceptual translation A;Residues: 1,17, 199, 102, A, 190, 1809, 1813, 1993 A;Title: The structure and complete nucleotide sequence of the murine gene encoding A;Residues: 1,17, 189, 102, 2005 A;Residues: 1,17, 189, 102, 2005 A;Residues: 1,17, 199, 102, 1985 A;Cross : references: EML/U04269; NID:940733; PMID:803421 D;Reference mamber: A5264; MUID:940733; PMID:803421 D;Reference number: A5264; MUID:940733; PMID:9476218 A;Cross : references: EML/U04269; Corp. 247.5; DB 2; Length 402; Molecular type DMA A;Cross : references: EML/U04269; Corp. 247.5; DB 2; Length 402; Molecular type DMA A;Cross : references: EML/U04269; Corp. 247.5; DB 2; Length 402; Molecular type DMA A;Cross : references: EML/U042

Qy 274 YFY 276 | : Db 397 YLF 399

Search completed: December 2, 2002, 12:57:09 Job time: 17.2828 secs

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Result
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Maximum DB
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            Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.
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          Gapext 0.5
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P06241 homo sapien	FYN_HUMAN		536	6.0	ä	45
P39688 mus m	FYN_MOUSE	μ,	533	5.2	90.5	44
068006 b bacitraci	BACA_BACLI	ب	5255	6.3	92.5	43
Q05876 gallus	FYN_CHICK	L	533	6.4	93	42
P27446 xiphor	FYN_XIPHE	٢	536	6.6	96	41
015519 h casp	CFLA_HUMAN	μ.	480	12.5	183	40
035732 m cas _l	CFLA_MOUSE	μ.	484	13.8	202	39
Q9n2il sus scrofa	I1BC_PIG	1	404	14.6	213.5	38
P70343 mus m	ICEB_MOUSE	ب	373	14.9	217.5	37
P29466 homo:	I1BC_HUMAN	_	404	15.2	222.5	36
P51878 homo s	ICE5_HUMAN	_	418	15.9	232.5	ر ان د
Q9mzv7 canis	I1BC_CANFA	ب	404	16.0	234.5	4

ALIGNMENTS

RP RA	R R I	R R	RA	R R A	RP	RRL	집 집	RA A	RA S	R X	Z Z	R.	작건	RT	RA	RX	R.P	RL	RT	RT Z	RA RA	RX	R RP	RN C	28	2 2	GN	DE	DE L	1 1 1	AC	RESULT ICE3_H ID I
X-RAY CRYSTALLOGRAPHY (2.3 ANGSTROMS) OF 35-173 AND 185-277. MEDLINE-97197830; Pubmed-9045680; Mittl P.R., di Marco S., Krebs J.F., Bai X., Karanewsky D.S.,	Nat. Struct. Biol. 3:619-625(1996).	dimensional:	M., Peterson E.P., Rasper D.M., Ruel R., Vaillancon	Gallant w	AY CRYSTALLOGRA		"Identification and inhibition of the ICE/CED-3 protease necessary for mammalian apoptosis.";	Smulson M.E., Yamin TT., I	t M., Gareau Y., G	d=7596430;	AND 175-193	Cell 81:801-809(1995).	cleaves the death substrate poly(ADP-ribose).	"Yama/CPP32 beta, a mammalian homolog of CED-3, is a CrmA-inhibitable	Tewari M., Quan L.T., O'Rourke K., Desnoyers S., Zeng Z., Beidler D.R., Poirier G.G., Salvesen G.S., Dixit V.M.:	MEDLINE=95292347; PubMed=7774019;	SEQUENCE FROM N.A.	J. Biol. Chem. 269:30761-30764(1994).	in-1 beta-converting enzyme.";	Caenorhabditis elegans cell death protein Ced-3 and mammalian	ri E.S.;	MEDLINE=95074098; PubMed=7983002;	UENCE FROM	\C51_1ax10=9000;	ia; Primates; Catarrhini; Hominidae; Homo.). Chordata: Craniata:		protein) (CPP-32) (Caspase-3) (CASP-3) (SREBP cleavage activity 1)	<pre>(Rel. 41, Last annotation update) ursor (EC 3.4.22) (Cysteine protease CPI</pre>	01-NOV-1995 (Rel. 32, Created) 01-NOV-1995 (Rel. 32, Last sequence update)		JCE3 HUMAN STANDARD: PRT: 277 AA

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Lee D., Long S.A., Adams J.L., Chan G., Vaidya K.S., Francis T.A.,
Kikly K., Winkler J.D., Sung C.-M., Debouck C., Richardson S.,
Kikly K., DeWolf W.E. Jr., Keller P.M., Tomaszek T., Head M.S.,
Ryan M.D., Haltiwanger R.C., Liang P.-H., Janson C.A., McDevitt P.J.,
Johanson K., Concha N.O., Chan W., Abdel-Meguid S.S., Badger A.M.,
Lark M.W., Nadeau D.P., Suva L.J., Gowen M., Nuttall M.E.;
"Potent and selective nonpeptide inhibitors of caspases 3 and 7
inhibit apoptosis and maintain cell functionality.";
Biol. Chem. 275:16007-16014(2000).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  MEDLINE=96331285; PubMed=8696339;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         "In vitro activation of CPP32 and Mch3 by Mch4, a novel human apoptotic cysteine protease containing two FADD-like domains. Proc. Natl. Acad. Sci. U.S.A. 93:7464-7469(1996).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Fernandes-Alnemri T., Armstrong R.C., Krebs J., Wang L., Bullrich F., Fritz L.C., Trapani J.A., Litwack G., Alnemri E.S.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 CLEAVAGE OF HUNTINGTIN
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Priestle J.P., Tomaselli K.J., Grutter M.G.;
"Structure of recombinant human CPP32 in complex
tetrapeptide acetyl-Asp-Val-Ala-Asp fluoromethyl
J. Biol. Chem. 272:6539-6547(1997).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  8
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     5
                                                                                                                                                                                                                                               TISSUE SPECIFICITY: HIGHLY EXPRESSED IN LUNG, SPLEEN, HEART, LIVER AND KIDNEY. MODERATE LEVELS IN BRAIN AND SKELETAL MUSCLE, AND LOW IN TESTIS. ALSO FOUND IN MANY CELL LINES, HIGHEST EXPRESSION IN CELLS OF THE IMMUNE SYSTEM.

PTM: CLEAVAGE BY GRANZYME B, APAF-1, CASPASE-6, -8 AND -10 GENERATES THE TWO ACTIVE SUBUNITS. ADDITIONAL PROCESSING OF THE PROPEPTIDES IS LIKELY DUE TO THE AUTOCATALYTIC ACTIVITY OF THE ACTIVATED PROTEASE. ACTIVE HETERODIMERS BETWEEN THE SMALL SUBUNIT OF CASPASE-7 PROTEASE AND THE LARGE SUBUNIT OF CPP32 ALSO OCCUR
                                                                                                                                                                 s SWISS-PROT entry is copyright. It is produced through a cemen the Swiss Institute of Bioinformatics and the EMBL European Bioinformatics Institute. There are no restrict
                                                                                                                                                                                                                            SIMILARITY: BELONGS
                        1CP3;
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                                                 U13737; AAA65015.1; -. U13738; AAB60355.1; -. U26943; AAA74929.1; -. 1PAU; 07-JUL-97.
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                                                                                                                                                                                                                                         VICE VERSA
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                        .23-JUN-00.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    a proapoptotic cysteine protease,
ract.";
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                                                                                                                                                        as its content
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Tomaselli K
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                                                                                                                                                                    restrictions
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K.J.,
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                                                                                                                                           for
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ICE3_RAT
ID ICE3
AC P523
AC P523
AC P524
DT 01-C
DT 15-C
DE Apoul
DE (SC)
DG RAT
OC Euk
OC Euk
OC Mamm
OX NCB
RN [1]
RP SE0
RN [2]
RP SE0
RX MED
RX MED
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Best Local
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InterPro; IPR002138; ICE_p10.
InterPro; IPR001309; ICE_p20.
Pfam; PF00655; ICE_p10; 1.
Pfam; PF00656; ICE_p20; 1.
PRINTS; PR00376; IL1BCENZYME.
SMART; SM00115; CASC; 1.
                                                                                                                                                             ICE3_RAT STANDARD; PRT; 277 AA.

P55213; P70543; Q62993; P97699;
01-OCT-1996 (Rel. 34, Created)
01-NOV-1997 (Rel. 35, Last sequence update)
15-JUN-2002 (Rel. 41, Last annotation update)
15-JUN-2002 (Rel. 41, Last annotation update)
Apopain precursor (EC 3.4.22.-) (Cysteine protease CPP32) (Yama protein) (CPP-32) (Caspase-3) (CASP-3) (SREBP Cleavage activity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    CHAIN
CHAIN
ACT_SITE
ACT_SITE
                                            Fletcher F.A.
                                                      Juan T.S.-C., McNiece
                                                                SEQUENCE FROM N.A. MEDLINE-96358624;
                                                                                                          Eukaryota; Metazoa;
Mammalia; Eutheria;
                     Molecular characterization cysteine protease resembli
                                                                                                NCBI_TaxID=10116;
                                                                                                                                Rattus norvegicus (Rat)
                                                                                                                                            CASP3 OR CPP32
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    PROSITE; PS01122; CASPASE CYS; PROSITE; PS01121; CASPASE_HIS; PROSITE; PS50207; CASPASE_P10; PROSITE; PS50208; CASPASE_P20;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     SEQUENCE
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            cysteine protease
nd CED-3.";
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                                                                                                                                                                                                                                                                                                                                                                                                                    MTSRSGTDVDAANLRETFRNLKYEVRNKNDLTREEIVELMRDVSKEDHSKRSSFVCVLLS
                                                                                                                                                      (LICE)
 13:749-755(1996)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Similarity
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                                                                PubMed=8761296;
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                                                                                                          Chordata;
Rodentia;
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                    of mouse and rating interleukin-1
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                                                      Jenkins
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APOPAIN P12 SU
BY SIMILARITY.
BY SIMILARITY.
D. -> E (IN ISO
                                                                                                       Craniata; Veri
Sciurognathi;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Score 1460;
Pred. No. 1
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Mismatches
                                                      N.A.,
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  1.7e-115;
                                                                                                                    Vertebrata;
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                                                     Gilbert
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               DB
                                                                                                                                                                                                                                                                                     277
                                                                                                           Muridae;
                     beta
                               CPP32 beta gene
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                                                     D.J.,
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                    converting
                                                                                                                     Euteleostomi;
                                                                                                          Murinae; Rattus.
                                                     Copeland
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                    enzyme
                                encoding
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Pfam; PFUVUL;
PRINTS; PR00376; IL18CB...
SMART; SM00115; CASC; 1.
PROSITE; PS011121; CASPASE_US; 1.
PROSITE; PS01121; CASPASE_HIS; 1
PROSITE; PS50207; CASPASE_P10; 1
PROSITE; PS50208; CASPASE_P20; 1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               use by modified
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between
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-i- FUNCTION: INVOLVED IN THE ACTIVATION CASCADE OF CASPASES
RESPONSIBLE FOR APOPTOSIS EXECUTION. AT THE ONSET OF APOPTOSIS IT
PROTECLYTICALLY CLEAVES POLYAGEN POLYMERASE (PARP) AT A
216-ASP-1-GLY-217 BOND. CLEAVES AND ACTIVATES STEROL REGULATORY
ELEMENT BINDING PROTEINS (SREBPS) BETWEEN THE BASIC HELIX-LOOP-
HELIX LEUCINE 2IPPER DOMAIN AND THE MEMBRANE ATTACHMENT DOMAIN.
CLEAVES AND ACTIVATES CASPASE-6, -7 AND -9 (BY SIMILARITY).

-i- SUBUNIT: HETERODIMER OF A 17 kDa (P17) AND A 12 kDa (P12) SUBUNIT
                                                                                                                                                                                         InterPro; IPR002398; ICE_D10.
InterPro; IPR002138; ICE_D10.
InterPro; IPR001309; ICE_D20.
Pfam; PF00655; ICE_D10; I.
Pfam; PF00656; ICE_D20; 1.
                                                                                                                                                                                                                                                                                                                                                                                                               EMBL;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                      EMBL;
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or send an email to license@isb-sib.ch).
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Ni B., Wu X., Du Y., Su Y., Hamilton-Byrd E., Rockey P.K.,
Rosteck P. Jr., Poirier G.G., Paul S.M.;
"Cloning and expression of a rat brain interleukin-lbeta-converting
enzyme (ICE)-related protease (IRP) and its possible role in
apoptosis of cultured cerebellar granule neurons.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Flaws J.A., Kugu K., Trbovich A.M., Desanti A., Tilly K.I., Hirshfield A.N., Tilly J.L.;
"Interleukin-1 beta-converting enzyme-related proteases (IRPs) and mammalian cell death: dissociation of IRP-induced oligonucleosomal endonuclease activity from morphological apoptosis in granulosa cells of the ovarian follicle.";
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Neurosci. 17:1561-1569(1997).
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(BY SIMILARITY).

SUBCELLULAR LOCATION: Cytoplasmic.

TISSUE SPECIFICITY: EXPRESSED IN HEART, BRAIN, LIVER, AND MUSCLE BUT NOT IN KIDNEY OR TESTIS.

DEVELOPMENTAL STAGE: HIGHLY EXPRESSED IN NEURON-ENRICHED REGIONS OF THE DEVELOPING BRAIN, BUT DOWN-REGULATED TO LOW LEVELS IN THE
                                                                                                                                                                                                                                                                                                                                                       L; U49930; AAC52765.1; -.
L; U34685; AAC52261.1; -.
L; U84410; AAB41792.1; -.
L; U58656; AAB02722.1; -.
P; P42574; IPAU.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 s SWISS-PROT entry is copyright. It is produced through ween the Swiss Institute of Bloinformatics and the Exeuropean Bioinformatics Institute. There are no restr
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             VICE VERSA (BY SIMILARITY).
SIMILARITY: BELONGS TO PEPTIDASE FAMILY C14.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 "FIM: CLEAVAGE BY GRANZYME B, CASPASE-6, -8 AND -10 GENERATES: TWO ACTIVE SUBUNITS. ADDITIONAL PROCESSING OF THE PROPEPTIDES LIKELY DUE TO THE AUTOCATALYTIC ACTIVITY OF THE ACTIVATED PROTEASE. ACTIVE HETERODIMERS BETWEEN THE SMALL SUBUNIT OF CASPASE-7 PROTEASE AND THE LARGE SUBUNIT OF CPP32 ALSO OCCUR AVIOLENCE AND THE LARGE SUBUNIT OF CPP32 ALSO OCCUR AVIOLENCE AND THE LARGE SUBUNIT OF CPP32 ALSO OCCUR AVIOLENCE AND THE LARGE SUBUNIT OF CPP32 ALSO OCCUR AVIOLENCE AND THE LARGE SUBUNIT OF CPP32 ALSO OCCUR AVIOLENCE AND THE LARGE SUBUNIT OF CPP32 ALSO OCCUR AVIOLENCE AND THE LARGE SUBUNIT OF CPP32 ALSO OCCUR AVIOLENCE AND THE LARGE SUBUNIT OF CPP32 ALSO OCCUR AVIOLENCE AND THE LARGE SUBUNIT OF CPP32 ALSO OCCUR AVIOLENCE AND THE LARGE SUBUNIT OF CPP32 ALSO OCCUR AVIOLENCE AND THE ACTIVATED AND THE LARGE SUBUNIT OF CPP32 ALSO OCCUR AVIOLENCE AND THE ACTIVATED AND THE LARGE SUBUNIT OF CPP32 ALSO OCCUR AVIOLENCE AND THE ACTIVATED AND THE A
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    non-profit institutions as long and this statement is not removed.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              CLEAVAGE BY GRANZYME
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           136:5042-5053(1995).
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Best Local 9
CPP32 during apoptosis.";
EMBO J. 15:1012-1020(1996).
-i- FUNCTION: INVOLVED IN THE ACTIVATION CASCADE OF CASPASES
-i- FUNCTION: INVOLVED IN THE ACTIVATION AT THE ONSET OF APOPTOSIS
RESPONSIBLE FOR APOPTOSIS EXECUTION. AT THE ONSET OF APOPTOSIS
PROTECLYTICALLY CLEAVES POLY(ADP-RIBOSE) POLYMERASE (PARP) AT A
216-ASP-[-GLY-217 BOND. CLEAVES AND ACTIVATES STEROL REGULATORY
                                                                                 Wang X., Zelenski
Goldstein J.L.;
                                                                                                                                                                 Cricetulus longicaudatus (Long-tailed hamster) (Chinese hamster)
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Cricetinae;
                                                                                                                                                                                                                                                                            ICE3_CRILO
Q60431;
                                                                                                                                                                                                                                                                                                  _CRILO
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                                                                "Cleavage of sterol regulatory
                                                                                                       MEDLINE=96183185;
                                                                                                                           SEQUENCE FROM
                                                                                                                                                                                                   CASP3 OR CPP32.
                                                                                                                                                                                                                       Apopain precursor protein) (CPP-32)
                                                                                                                                                                                                                                           01-NOV-1997 (Rel.
01-NOV-1997 (Rel.
15-JUN-2002 (Rel.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               CHAIN
ACT_SITE
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                                                                                                                                                             Cricetulus
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                                                                                                                                                                                                                  35, Created)
35, Last sequence update)
41, Last annotation update)
(EC 3.4.22.-) (Cysteine protease CPP32) (Yama (Caspase-3) (CASP-3) (SREBP cleavage activity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             protease;
                                                                                                      PubMed=8605870;
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89.2%;
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                                                                                          J.,
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T -> 2
H -> 1
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Pred. No. 1.8e-103;
3; Mismatches 17;
                                                                                                                                                                              Craniata; Vertebrata; Euteleostomi;
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BY SIMILARITY.
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                                                                                          Sakai J.,
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> V (IN REF. 2).
> V (IN REF. 2).
> K (IN REF. 2).
> K (IN REF. 2).
> G (IN REF. 3).
> G (IN REF. 2).
> J (IN REF. 4).
> M (IN REF. 3).
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Best Local S
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InterPro; IPR002138; ICE_p10.
InterPro; IPR0011309; ICE_p20.
InterPro; IPR001309; ICE_p20; 1.
Pfam; PF00655; ICE_p10; 1.
Pfam; PF00656; ICE_p20; 1.
PRINTS; PR00376; ILIBCENZYME.
SMART; SM00115; CASC; 1.
                                                                                                                                                                                                                                                                                                                                                                                            ACT_SITE
ACT_SITE
SEQUENCE
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PROSITE: PS01121; CASPASE_HIS; 1.
PROSITE: PS50207; CASPASE_P10; 1.
PROSITE: PS50208; CASPASE_P20; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
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HSSP; P42574;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      PTM: CLEAVAGE BY GRANZYME B, CASPASE-6, -8 AND -10 GENERATES TWO ACTIVE SUBUNITS. ADDITIONAL PROCESSING OF THE PROPERTIDES LIKELY DUE TO THE AUTOCATALYTIC ACTIVITY OF THE ACTIVATED PROTEASE. ACTIVE HETERODINERS BETWEEN THE SMALL SUBUNIT OF CASPASE-7 PROTEASE AND THE LARGE SUBUNIT OF CPP32 ALSO OCCUR VERSA (BY SIMILARITY).

SIMILARITY: BELONGS TO PEPTIDASE FAMILY C14.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ELEMENT BINDING PROTEINS (SREBPS) BETWEEN THE BASIC HELIX-LOOP-HELIX LEUCINE ZIPPER DOMAIN AND THE MEMBRANE ATTACHMENT DOMAIN CLEAVES AND ACTIVATES CASPASE-6, -7 AND -9 (BY SIMILARITY).

SUBUNIT: HETERODIMER OF A 17 kDa (P17) AND A 12 kDa (P12) SUBUN
                                                                RKVATEFESFSLDSTFHAKKQIPCIVSMLTKELYFYH
                                                                            RKVATEFESFSFDATFHAKKQIPCIVSMLTKELYFYH 277
                                                                                                                             DMACHKIPVEADFLYAYSTAPGYYSWRNSKDGSWFIQSLCAMLKQYADKLEFMHILTRVN
                                                                                                                                                                                                                        MTPRSGTDVDAAKLRETFMALKYEVRNKNDLTREEIVELMKNASKEDHSKRSSFVCVILS
                                                                                                                                                                                                                                                                            MENNETSYDSKSIKNFEYKTIHGSKSMDSGIYLDSSYKMDYPEMGYCIIINNKNFHKSTG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        (BY SIMILARITY).
SUBCELLULAR LOCATION: Cytoplasmic.
                                                                                                                HGEEGIIFGTNGPVDLKKITNFFRGDRCRSLTGKPKLFIIQACRGTELDCGIETDSGVDD
                                                                                                                                                                                                                                       MTSRSGTDVDAANLRETFRNLKYEVRNKNDLTREEIVELMRDVSKEDHSKRSSFVCVLLS
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                                                                                                                                                                                                                                                                                                                                                    Similarity
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10
29
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163
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1 9 BY SIMILARITY.

0 28 BY SIMILARITY.

10 28 BY SIMILARITY.

11 175 APOPAIN P17 SUBUNIT.

12 BY SIMILARITY.

13 163 BY SIMILARITY.
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 STANDARD;
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87.0%;
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PRT;
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277
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Fernandes Alnemri T., Litwack G., Alnemri E.S.;

Submitted (MAY-1997) to the EMBL/GenBank/DBBJ databases.

11 FUNCTION: INVOLVED IN THE ACTIVATION CASCADE OF CASPASES

RESPONSIBLE FOR APOPTOSIS EXECUTION. AT THE ONSET OF APOPTOSIS IT PROTEDLYTICALLY CLEAVES POLY(ADP-RIBOSE) POLYMERASE (PARP) AT A 216-ASP-1-GLY-217 BOND. CLEAVES POLY(ADP-RIBOSE) POLYMERASE (PARP) AT A 215-ASP-1-GLY-217 BOND. CLEAVES AND ACTIVATES STEROL REGULATORY ELEMENT BINDING PROTEINS (SREBPS) BETWEEN THE BASIC HELIX'LOOP-HELIX LEUCINE ZIPPER DOMAIN AND THE MEMBRANE ATTACHMENT DOMAIN. CLEAVES AND ACTIVATES CASPASE-6, 77 AND -9 (BY SIMILARITY).

CLEAVES AND ACTIVATES CASPASE-6, 77 AND AN ALA, RELEASTING THE MATURE CYTOKINE WHICH IS INVOLVED IN A VARIETY OF INFLAMMATORY PROCESSES.

-1- SUBUNIT: HETERODIMER OF A 17 kDa (P17) AND A 12 kDa (P12) SUBUNIT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 P70677; 008668;
01-NOV-1997 (Rel. 3
01-NOV-1997 (Rel. 3
15-JUN-2002 (Rel. 4
                                                                                                                                                                                                                                                              ++
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           SEQUENCE FROM
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  MEDLINE=97190206; PubMed=9038361; van de Craen M., Vandenabeele P., van Loo G., Molemans F., Schotte
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Biochem.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                NGF.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Mukasa T., Urase K., Momoi M.Y., Kimura I., Momoi T.; "Specific expression of CPP32 in sensory neurons of mouse embry activation of CPP32 in the apoptosis induced by a withdrawal of
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       a cysteine protease resembling
and CED-3.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             MEDLINE=96358624; PubMed=8761296;
Juan T.S.-C., McNiece I.K., Jenki
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Mus musculus (Mouse).
Eukaryota; Metazoa; Chordata;
Mammalia; Eutheria; Rodentia;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Apopain precursor protein) (CPP-32) (SCA-1) (LICE).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       "Characterization of seven murine FEBS Lett. 403:61-69(1997).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Fiers W.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         MEDLINE=97224429; PubMed=9070890;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Oncogene 13:749-755(1996).
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                                                                                                             PTM: CLEAVAGE BY GRANZYME B, CASPASE-6, -8 AND -10 GENERAY TWO ACTIVE SUBUNITS. ADDITIONAL PROCESSING OF THE PROPEPTI LIKELY DUE TO THE AUTOCATALYTIC ACTIVITY OF THE ACTIVATED PROTEASE. ACTIVE HETERODIMERS BETWEEN THE SMALL SUBUNIT OF CASPASE-7 PROTEASE AND THE LARGE SUBUNIT OF CP93 ALSO OCC VICE VERSA (BY SIMILARITY).
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SUBCELLULAR LOCATION: Cytoplasmic.
TISSUE SPECIFICITY: HIGHEST EXPRESSION IN SPI
TISSUE SPECIFICITY: LOWER EXPRESSION IN BRAIN,
                                                                  SWISS-PROT entry is copyright. It is produced through een the Swiss Institute of Bioinformatics and the EN
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35, Last sequence update)
41, Last annotation update)
(EC 3.4.22.-) (Cysteine protease CPP32) (Yama (Caspase-3) (CASP-3) (SREBP cleavage activity 1)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Res. Commun. 231:770-774(1997)
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interleukin-1
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P., van Criekinge W., Beyaert
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RESULT
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             ICE3_XENLA STANDARD; PR
P55866;
01-NOV-1997 (Rel. 35, Created)
01-NOV-1997 (Rel. 35, Last seque
15-JUN-2002 (Rel. 41, Last annot
Apopain precursor (EC 3.4.22.-)
(CASP-3) (XCPP32).
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InterPro; IPR002338; ICE_P10.
InterPro; IPR002138; ICE_P10.
InterPro; IPR001309; ICE_P20.
Pfam; PF00655; ICE_P10; 1.
Pfam; PF00655; ICE_P20; 1.
PRINTS; PR00376; ILIBCENZYME.
SMART; SM00115; CASC; 1.
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EMBL; D86352;
EMBL; Y13086;
EMBL; U19522;
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            CASP3
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PROPEP
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PROSITE: PS01121; CASPASE_HIS; 1.
PROSITE: PS50207; CASPASE_P10; 1.
PROSITE: PS50208; CASPASE_P20; 1.
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                                                                                             MENTENSYDSKSIKNLEPKIIHGSESMDSGISLDNSYKMDYPEMGLCIIINNKNFHKSTG
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                                                                                                                               DMACHKIPVEADFLYAYSTAPGYYSWRNSKDGSWFIOSLCAMLKQYADKLEFMHILTRVN 240
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U54802;
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AAC52764.1;
BAA21727.1;
CAA73528.1;
AAC53196.1;
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                      Last sequence update)
Last annotation updat
3.4.22.-) (Cysteine p
  clawed frog).
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                                                                                                                                                                                                                                               Score 1293;
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                                                                                                                                                                                                                                                                                                                          APOPAIN P17 SUBUNIT APOPAIN P12 SUBUNIT BY SIMILARITY BY SIMILARITY.
                                                                                                                                                                                                                                                                                                                                                       BY SIMILARITY.
BY SIMILARITY.
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                                                           282
                               update)
                                                                                                                                                                                                                                        .8e-101;
les 17;
                                                          8
                      protease CPP32) (Caspase-3)
                                                                                                                                                                                                                                                      DB 1;
                                                                                             277
                                                                                                           277
                                                                                                                                                                                                                                                                    CRC64;
                                                                                                                                                                                                                                                     Length
                                                                                                                                                                                                                                        Indels
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Best Local S
Matches 156
                                                                                                                                                        CHAIN
ACT_SITE
ACT_SITE
SEQUENCE
                                                                                                                                                                                     CHAIN
              180
                                                                                                                                                                                            PROPEP
                                                                                                                                                                                                   Hydrolase;
                            169
                                                                                                                                                                                                                                                                  InterPro;
                                                                                                                                                                                                                                                                         InterPro;
                                                                                                                                                                                                                                                                               InterPro;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Yaoita Y.,
229
                                          120
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SMART; SM00115; CASC; 1.
PROSITE; PS01122; CASPASE_CYS; 1.
PROSITE; PS01121; CASPASE_HIS; 1.
PROSITE; PS0207; CASPASE_P10; 1.
PROSITE; PS0208; CASPASE_P20; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Pfam; PF00655; ICE_p10; Pfam; PF00656; ICE_p20;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   -I- FUNCTION: IMPORTANT MEDIATOR OF APOPTOSIS. AT THE ONSE APOPTOSIS IT PROTEOLYTICALLY CLEAVES POLY(ADP-RIBOSE) (PARP) AT A 216-ASP-|-GLY-217 BOND (BY SIMILARITY).
-I- SUBUNIT: HETERODIMER OF A 17 kDa (P17) AND A 12 kDa (F SUBUNITS.
-I- SUBCELLAUGUS: THE SUBUNITS ARE DERIVED FROM THE PRECU
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            "Induction of apoptosis and CPP32 myoblastic cell line derived from J. Biol. Chem. 272:5122-5127(1997)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                EMBL; D89784; BAA14018.1; -. HSSP; P42574; 1PAU.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                MEROPS; C14.003;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       -!- SIMILARITY: BELONGS TO PEPTIDASE FAMILY C14.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     MEDLINE-97184166;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Amphibia; Batrachia;
Xenopodinae; Xenopus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Eukaryota;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           MISCELLANEOUS: THE SUBJUNITE SEQUENCE BY A PROBABLE AUTOCATALYTIC SEQUENCE BY A PROBABLE AUTOCATALYTIC STREET CASPASES (BY SIMILARITY).
KLEFMHILTRVNRKVATEFESFSFDATFHAKKQIPCIVSMLTKELYFY
                                        DSGIETDSCSEPREEIQRIPVEADFLYAYSTVPGYCSWRDKMDGSWFIQSLCKMIKLYGS
                                                                DCGIETDSGVDDDMACHKIPVEADFLYAYSTAPGYYSWRNSKDGSWFIQSLCAMLKQYAD
                                                                                                                           KRSSFVCAILSHGEEDGSICGVDVPIHIKNLTDLFRGDRCKTLVGKPKIFFIQACRGTEL
                                                                                                                                                 KRSSFVCVLLSHGEE-GIIFGTNGPVDLKKITNFFRGDRCRSLTGKPKLFIIQACRGTEL
                                                                                                                                                                                                                                             INNKNFHKSTGMTSRSGTDVDAANLRETFRNLKYEVRNKNDLTREEIVELMRDVSKEDHS
                                                                                                                                                                                                                  INNKNFH-SSNMAVRNGTDVDALKLHETFTGLGYEVMVCNDQKSSDIIGRLKKISEEDHS
                                                                                                                                                                                                                                                                                                       MEESQNGVKYGGDATDAKEYFTIQPRSLQNCDLKDIERKTKFAHLQNYRTNYPEMGMCLI
                                                                                                                                                                                                                                                                                                                                                MENTENSV-----DSKSIKNLEPKIIHGSESMD----SGISLDNSYKMDYPEMGLCII 49
                                                                                                                                                                                                                                                                                                                                                                                                                     Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           IPR002138; ICE_p10.
IPR001309; ICE_p20
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        IPR002398;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Nakajima K.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Metazoa; Chordata; Craniata; Vertebrata;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 282
                                                                                                                                                                                                                                                                                                                                                                                               Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               protease;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 PubMed=9030578;
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                                                                                                                                                                                                                                                                                                                                                                                                              53.8%;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 MW;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Zymogén; Apopto:
BY SIMILARITY
                                                                                                                                                                                                                                                                                                                                                                                               40;
                                                                                                                                                                                                                                                                                                                                                                                          Score 786.5;
Pred. No. 6.1e
40; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   BY SIMILARITY
BY SIMILARITY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              APOPAIN P17 SUBUNIT APOPAIN P12 SUBUNIT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              CPP32 expression by thyroid from tadpole tail.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                             CB390E6980CAB77F CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Apoptosis
                                                                                                                                                                                                                                                                                                                                                                                                                .1e-59;
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                                                                                                                                                                                                                                                                                                                                                                                                                                       DΒ
                                                                                                                                                                                                                                                                                                                                                                                            73;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        PRECURSOR
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      hormone
                                                                                                                                                                                                                                                                                                                                                                                                                                     282;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 POLYMERASE
                                                                                                                                                                                                                                                                                                                                                                                            19;
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L outstation -
                                                                                                                                                                                                                                                                                                                                                                                          Gaps
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RESULT
ICE7_M
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                                                                                                                                                                                                                                 Submitted (MAR 2001) to the EMBL/GenBank/DDBJ databases.

11 FUNCTION: INVOLVED IN THE ACTIVATION CASCADE OF CASPASES RESPONSIBLE FOR APOPTOSIS EXECUTION. CLEAVES AND ACTIVATES STEROL REGULATORY ELEMENT BINDING PROTEINS (SREBPS). OVEREXPRESSION PROMOTES PROGRAMMED CELL DEATH (BY SIMILARITY).

11 SUBUNIT: HETERODIMER OF A 20 kDa (P20) AND A 11 kDa (P11) SUBUNIT.

12 SUBCELULLAR LOCATION: Cytoplasmic.

13 SUBCELULLAR LOCATION: Cytoplasmic.

14 TISSUE SPECIFICITY: HIGHLY EXPRESSED IN HEART, LUNG, LIVER, AND KIDNEY. LOW LEVELS IN SPLEEN, SKELETAL MUSCLE, AND TESTIS. NO
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                                                                                                                                                                                                                                                                                                                                                                                   Strausberg
                                                                                                                                                                                                                                                                                                                                                                                                                                   FEBS Lett.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              van de Craen M.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         MEDLINE-97190206; PubMed-9038361;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      differentiation
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        "Identification and mapping of Casp7, a cysteine CPP32 beta, interleukin-1 beta converting enzyme,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      MEDLINE=97224489; PubMed=9070923; Juan T.S.-C., McNiece I.K., Argento J.M., Jenkins N.A.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        SEQUENCE FROM N.A.
TISSUE-Skeletal muscle;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Mus musculus (Mouse).
Eukaryota; Metazoa; Chordata;
Mammalia; Eutheria; Rodentia;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        01-NOV-1997 (Rel. 35, Created)
01-NOV-1997 (Rel. 35, Last sequence update)
15-JUN-2002 (Rel. 41, Last annotation update)
Caspase-7 precursor (EC 3.4.22.-) (LICE2 cysteine
                                                                                                                                                                                                                                                                                                                                                                                                                                                              Fiers W.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                              van Loo G., Molemans
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Mukasa
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Genomics
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Copeland N.G., Fletcher F.A.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  protease Mch-3).
CASP7 OR MCH3 OR LICE2.
                                                                                                                                                                                                                                                                                                                                                                                                     SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                              "Characterization of
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Biochem. Biophys.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     "Wortmannin enhances CPP32-like activity differentiation of P19 embryonal carcinon
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               P97864; 008669;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                MEDLINE=97236307; PubMed=9125129;
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                                                                                                                            EXPRESSION IN THE BRAIN.

PTM: CLEAVAGES BY GRANZYME B OR CASPASE-10 GENERATE THE TWO ACTIVE SUBURITS. PROPERTIDE DOMAINS CAN ALSO BE CLEAVED EFFICIENTLY BY CP932 PROTEASE. ACTIVE HETERODIMERS BETWEEN THE SMALL SUBURIT OF CASPASE-7 AND THE LARGE SUBURIT OF CPP32 PROTEASE ALSO OCCUR AND VICE VERSA (BY SIMILARITY).

SIMILARITY: BELONGS TO PEPTIDASE FAMILY C14.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                MOUSE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        HLELIQILTCVNHMVALDFE--
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              40:86-93(1997).
                                                                                                                                                                                                                                                                                                                                                                                                                                   403:61-69(1997)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Khoroku
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             STANDARD;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Vandenabeele P.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Res.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Υ.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                             F.,
                                                                                                                                                                                                                                                                                                                                                                                                                                             seven murine caspase family members.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Commun.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Tsukahara
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Schotte
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Sciurognathi; Muridae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      232:192-197(1997).
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                T.,
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P., van Criekinge
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Momoi M.Y., Kimura
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     neuronal
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             protease) (Apoptotic
                                                                                                                                                                                                                                                                                                                                                                                                                                                                         den Brande I.,
W., Beyaert R.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Euteleostomi; 
Murinae; Mus
                                                                      restrictions
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                                                                                    a collaboration
                                        for
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                      .ch/announce/
                                                                                   outstation
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                                                                                                                                                                                          ICE7_MESAU
                                                                                                                                                                                                      RESULT
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Best Local
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Pfam; PF00656; ICE_p20; 1.

PRINTS; PR00376; ILIBCENZYME.

SMART; SM00113; CASC; 1.

PROSITE; PS01122; CASCASE_Y10; 1.

PROSITE; PS01121; CASCASE_HIS; 1.

PROSITE; PS01121; CASCASE_P10; 1.

PROSITE; PS50208; CASCASE_P20; 1.
                                                                                                                               P55214;
01-OCT-1996;
01-OCT-1996;
15-JUN-2002;
                                                                                                   01-0CT-1996 (Rel. 34, Created)
01-0CT-1996 (Rel. 34, Last sequence update)
15-JUN-2002 (Rel. 41, Last annotation update)
Caspase-7 precursor (EC 3.4.22.-) (ICE-11ke apoptotic protease
(ICE-LAP3) (Apoptotic protease Mch-3) (SREBP cleavage activity
                                   CASP/ OK MUTAL.

Mesocricetus auratus (Golden hamster).

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

Mammalia: Entheria; Rodentia; Sciurognathi; Muridae; Cricetinae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             PROPEP
CHAIN
ACT_SITE
ACT_SITE
CONFLICT
CONFLICT
CONFLICT
SEQUENCE
SEQUENCE FROM N.A.,
                    Mesocricetus.
NCBI_TaxID=10036;
                                                                                 CASP7 OR MCH3.
                                                                                                                                                                               ICE7_MESAU
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              MGD; MGI:109383; Casp7
InterPro; IPR002398; I
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       InterPro; IPR002138; ICE_p10
InterPro; IPR001309; ICE_p20
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               EMBL; Y13088; CF
EMBL; BC005428;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            CHAIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        PROPEP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Hydrolase;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        MEROPS;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    HSSP; P42574;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     EMBL; U67321; EMBL; D86353;
                                                                                                                                                                                                                                         300
                                                                                                                                                                                                                                                                274
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                                                                                                                                                                                                                                                                                                                                                                                                                                             37 YKMDYPEMGLCIIINNKNFHKSTGMTSRSGTDVDAANLRETFRNLKYEVRNKNDLTREEI 96
                                                                                                                                                                                                                                         ΥF
                                                                                                                                                                                                                                                               ΥŦ
                                                                                                                                                                                                                                                                                                   WFIQSLCAMLKQYADKLEFMHILTRVNRKVATEFESFSFDATFHAKKQIPCIVSMLTKEL
                                                                                                                                                                                                                                                                                                                                               LFIIQACRGTELDCGIETDSGVDDDMAC----HKIPVEADFLYAYSTAPGYYSWRNSKDGS
                                                                                                                                                                                                                                                                                                                                                                                               VELMRDVSKEDHSKRSSFVCVLLSHGEEGIIFGTNGFVDLKKITNFFRGDRCRSLTGKPK 156
                                                                                                                                                                                                                                                                                      WFVQALCSILNEHGKDLEIMQILTRVNDRVARHFESQSDDPRFNEKKQIPCMVSMLTKEL
                                                                                                                                                                                                                                                                                                                                                                                                                               YRMDFQKMGKCIIINNKNFDKATGMDVRNGTDKDAGALFKCFQNLGFEVTVHNDCSCAKM 119
                                                                                                                                                                                                                                                                                                                                                                                   QDLLRKASEEDHSNSACFACVLLSHGEEDLIYGKDGVTPIKDLTAHFRGDRCKTLLEKPK
                                                                                                                                                                                                                                                                                                                                    LFFIQACRGTELDDGIQADSGPINDIDANPRNKIPVEADFLFAYSTVPGYYSWRNPGKGS
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Similarity
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      BAA19730.1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              AA;
                                                                                                                                                                               STANDARD;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               AAH05428.1; -.
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11
45
49
 AND PARTIAL SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              34060 MW;
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59.5%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     BY SIMILARITY.

BY SIMILARITY.

BY SIMILARITY.

BY SIMILARITY.

CASPASE-7 SUBUNIT FOR SIMILARITY.

BY SIMILARITY.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 36;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Score 748.5;
Pred. No. 1e-5
36; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              BY SIMILARITY.
BY SIMILARITY.
EL -> DW (IN REF.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           -> T (IN REF. 2).
R -> RQ (IN REF. 2).
747787B5BDE5F744 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         No. 1e-55;
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                                                                                                                                                                             A
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      DB 1;
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<u>ب</u>

밁 VQ

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Matches 141;
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                                                                                                                                                                                                                                                                        Query Match
                                                                                                                                                                                                                                                                                                                     CHAIN
ACT_SITE
ACT_SITE
                                                                                                                                                                                                                                                                                                       SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                CHAIN
                                                                                                                                                                                                                                                                                                                                                                                                                     PROSITE: PS01122; CASPASE CYS; PROSITE; PS01121; CASPASE_HIS; PROSITE; PS50207; CASPASE_P10; PROSITE; PS50208; CASPASE_P20;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    EMBL;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/
                                                                                                                                                                                                                                                                                                                                                                 PROPEP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             InterPro; IPR002138; ICE_p;
InterPro; IPR001309; ICE_p;
Pfam; Pr00655; ICE_p10; 1.
Pfam; Pr00656; ICE_p20; 1.
                                                                                                                                                                                                                                                                                                                                                                                             Hydrolase;
PROPEP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 PRINTS; PR00376; ILIBO
SMART; SM00115; CASC;
       240
                                 214
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        MEROPS; C14.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                or send
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Pai J.-T., Brown M.S., Goldstein J.L.;
"Purification and cDNA cloning of a second apoptosis-related
protease that cleaves and activates sterol regulatory element
                                                               180
                                                                                          157
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                proteins.";
                                                                                                                       120
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        MEDLINE-96224303; PubMe
Pai J.-T., Brown M.S.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Proc
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                                                                                                                                                                                                               37
                                                                                                                                                                                                                                                            Local
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               (BY SIMILARITY).

(BY SIMILARITY).

SUBCELLULAR LOCATION: Cytoplasmic.

SUBCELLULAR LOCATION: Cytoplasmic.

SUBCELLULAR LOCATION: Cytoplasmic.

BY GRANZYME B OR CASPASE-10 GENERATE THE TWO ACTIVE SUBUNITS. PROPERTIDE DOMAINS CAN ALSO BE CLEAVED EFFICIENTLY BY CP932 PROTEASE. ACTIVE HETERODIMERS BETWEEN THE SMALL SUBUNIT OF CASPASE-7 AND THE LARGE SUBUNIT OF CP932 PROTEASE ALSO OCCUR AND CASPASE-7.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               C. Natl. Acad. Sci. U.S.A. 93:5437-5442(1996).
FUNCTION: INVOLVED IN THE ACTIVATION CASCADE OF CASPASES
RESPONSIBLE FOR APOPTOSIS EXECUTION. CLEAVES AND ACTIVATES STEROL
REGULATORY ELEMENT BINDING PROTEINS (SREBPS). PROTEOLYTICALLY
CLEAVES POLY(ADP-RIBOSE) POLYMERASE (PARP) AT A 216-ASP-1-GLY-217
BOND. OVEREXPRESSION PROMOTES PROGRAMMED CELL DEATH (BY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   VICE VERSA (BY SIMILARITY).
SIMILARITY: BELONGS TO PEPTIDASE FAMILY
               WFIQSLCAMLKQYADKLEFMHILTRVNRKVATEFESFSFDATFHAKKQIPCIVSMLTKEL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             BOND. OVEREXPRESSION PROMOSIMILARITY).
SUBUNIT: HETERODIMER OF A
(BY SIMILARITY).
WFVQALCSILDEHGKDLEIMQILTRVNDRVARHFESQCDDPCFNEKKQIPCMVSMLTKEL
                                                                        LFIIQACRGTELDCGIETDSG----VDDDMACHKIPVEADFLYAYSTAPGYYSWRNSKDGS
                                                                                                                                    YRMDFEKMGKCIIINNKNFDKVTGMDVRNGTDKDAEALFKCFRSLGFDVVVYNDCSCAKM
                                                                                                                                                                                             YKMDYPEMGLCIIINNKNFHKSTGMTSRSGTDVDAANLRETFRNLKYEVRNKNDLTREEI 96
                                                       LFFIQACRGTELDDGVQADSGPINETDANPRYKIPVEADFLFAYSTVPGYYSWRNPGKGS
                                                                                                                   QDLLRKASEEDHSNSACFACVLLSHGEENLIYGKDGVTPIKDLTAHFRGDRCKTLLEKPK
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        P42574;
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                                                                                                                                                                                                                                                         Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         IPR002398;
                                                                                                                                                                                                                                                                                                                                                                                                           Thiol
                                                                                                                                                                                                                                                                                                     186
303 AA;
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199
207
144
                                                                                                                                                                                                                                           Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                           protease;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 IL1BCENZYME
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       PubMed=8643593;
                                                                                                                                                                                                                                                                                                                                 198
206
303
144
                                                                                                                                                                                                                                                                                                     34037 MW;
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                                                                                                                                                                                                                                                          58
                                                                                                                                                                                                                                                         .38;
                                                                                                                                                                                                                                         35;
                                                                                                                                                                                                                                                                                                                                                                                                        Zymogen;
                                                                                                                                                                                                                                                       Score
Pred.
                                                                                                                                                                                                                                                                                                                   BY
BY
                                                                                                                                                                                                                                                                                                                                             CASPASE-7 SUBUNIT
BY SIMILARITY
CASPASE-7 SUBUNIT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     20 kDa (P20) AND A 11 kDa (P11) SUBUNIT
                                                                                                                                                                                                                                                                                                  EA29356D90984648 CRC64;
                                                                                                                                                                                                                                                                                                                   SIMILARITY.
                                                                                                                                                                                                                                         Mismatches
                                                                                                                                                                                                                                                         726.5;
No. 7.:
                                                                                                                                                                                                                                                                                                                                                                                                        Apoptosis
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                                                                                                                                                                                                                                                                     DB 1;
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 299
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RESULT 8
ICE7_HUMAN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ICE7.HUMAN STANDAKU;
P55210; Q13364; Q96BAO;
O1-CCT-1996 (Rel. 34, Created)
O1-CCT-1996 (Rel. 34, Last sequence update)
15-JUN-2002 (Rel. 41, Last annotation update)
Caspase-7 precursor (EC 3.4.22.-) (ICE-like apoptotic
          apoptotic cysteine protease containing two FADD-like domains.";
Proc. Natl. Acad. Sci. U.S.A. 93:7464-7469(1996).
-i- FUNCTION: INVOLVED IN THE ACTIVATION CASCADE OF CASPASES
RESPONSIBLE FOR APOPTOSIS EXECUTION. CLEAVES AND ACTIVATES
                                                                                                                                                                                                                  "Identification and mapping of Casp7, a cysteine protease resembling CPP32 beta, interleukin-1 beta converting enzyme, and CED-3.";
                                                                                                                                                                                                                                            Juan T.S.-C., McNiece I.K., Argento J.M.,
Copeland N.G., Fletcher F.A.;
                                                         Fernandes-Alnemri T., Armstrong R.C., Krebs J., Wang L., Bullrich F., Fritz L.C., Trapani J.A., Litwack G., Alnemri E.S.;
"In vitro activation of CPP32 and Mch3 by Mch4,
                                                                                                                                                           Strausberg
                                                                                                                                                                                                                                                                   TISSUE=Fetal lung, and Fetal spleen; MEDLINE=97224489; PubMed=9070923;
                                                                                                          PROCESSING.
MEDLINE=96353838;
                                                                                                                                                Submitted
                                                                                                                                                                      TISSUE-Skin;
                                                                                                                                                                                   SEQUENCE FROM
                                                                                                                                                                                                                                                                                                                                  CPP32
                                                                                                                                                                                                                                                                                          SEQUENCE FROM N.A. (ALPHA AND ALPHA'
                                                                                                                                                                                                                                                                                                                                   "Mch3, a novel human apoptotic cysteine CPP32.";
                                                                                                                                                                                                                                                                                                                                                                    Fritz L.C
                                                                                                                                                                                                                                                                                                                                                                             Fernandes-Alnemri
                                                                                                                                                                                                                                                                                                                                                                                                       TISSUE=T-cel
                                                                                                                                                                                                                                                                                                                                                                                                                                       Lippke J.A., Gu Y., Sarnecki C., Carol
"Identification and characterization or
cysteine protease similar to CPP32.",
J. Biol. Chem. 271:1825-1828(1996).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      MEDLINE=96147144;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              SEQUENCE FROM N.A. (ALPHA ISOFORM). MEDLINE-96139498; PubMed-8576161;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Eukaryota; Metazoa;
Mammalia; Eutheria;
                                                                                                                                                                                                                                                                                                                                                      Earnshaw W.C.,
                                                                                                                                                                                                                                                                                                                                                                                         MEDLINE=96105019; PubMed=8521391;
                                                                                                                                                                                                                                                                                                                                                                                                                 SEQUENCE FROM N.A. (ALPHA AND BETA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     TISSUE-Spleen;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  cell
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          "ICE-LAP3, a novel mammalian homologue
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Dixit V.M.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Duan H.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Homo sapiens (Human).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 cell death protein Ced-3 factor-induced apoptosis
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                                                                                                                                                                                                 beta, interreus...
ics 40:86-93(1997).
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Chinnaiyan
                                                                                                                                                                                                                                                                                                                                                     -Alnemri T., Takahashi A., A
., Tomaselli K.J., Wang L.,
W.C., Litwack G., Alnemri E.
                                                                                                                                               (OCT-2001)
                                                                                                                                                           æ
                                                                                                                                                                                                                                                                                                                  55:6045-6052(1995).
                                                                                                                                                                                  N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              N.A. (ALPHA ISOFORM).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      apoptosis.";
271:1621-1625(1996)
                                                                                                           PubMed=8755496;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        PubMed=8567622;
                                                                                                                                                                                  (ALPHA ISOFORM
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Chordata; Primates;
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                                                                                                                                                                                                                                                                                                                                                               Takahashi A., Armstrong R.C., Krebs K.J., Wang L., Yu Z., Croce C.M., Sa
                                                                                                                                             the
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        is activated
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                                                                                                                                             EMBL/GenBank/DDBJ databases
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Catarrhini;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Caron
                                                                                 .C., Krebs J.,
Trapani J.A.,
                                                                                                                                                                                                                                                                                                                                                                                                                ISOFORMS).
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          of the Caenorhabditis
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                                                                                                                                                                                                                                                                                                                                          protease highly related
                                                                                                                                                                                                                                                                                                                                                                                                                                                                CPP32/Mch2
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                                                           a
                                                                                  Srinivasula
Tomaselli K
                                                                                                                                                                                                                                                      N.A.,
PROTEOLYTICALLY
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                                                           novel
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                                                            human
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Query Match
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EMBL; U40281; AAC50352.1; --
EMBL; U37448; AAC50303.1; --
EMBL; U37449; AAC50304.1; --
EMBL; U67319; AAC51152.1; --
EMBL; U67320; AAC51153.1; --
                        CONFLICT
CONFLICT
SEQUENCE
                                                                                                                                                          PROPEP
CHAIN
ACT_SITE
ACT_SITE
VARSPLIC
                                                                                                                                                                                                                                                                                             Pfam; PF00655; ICE_p10; 1.
Pfam; PF00656; ICE_p20; 1.
PRINTS; PR00376; IL1BCENZYME.
SMART; SM00115; CASC; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                EMBL;
                                                          MUTAGEN
                                                                                                                                      VARSPLIC
                                                                                                                                                                                                                  CHAIN
                                                                                                                                                                                                                                                PROSITE; PS01122; CASPASE_CYS;
PROSITE; PS01121; CASPASE_H1S;
PROSITE; PS50207; CASPASE_P10;
PROSITE; PS50208; CASPASE_P20;
                                                                                                                                                                                                                                                                                                                                          InterPro; IPR002398;
InterPro; IPR002138;
InterPro; IPR001309;
                                                                                                                                                                                                                              PROPEP
                                                                                                                                                                                                                                         Hydrolase;
                                                                                                                                                                                                                                                                                                                                                                               MIM;
                                                                                                                                                                                                                                                                                                                                                                                      Genew; HGNC:1508; CASP7.
                                                                                                                                                                                                                                                                                                                                                                                                                                    EMBL;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             use by non-profit institutions as long as modified and this statement is not removed. \ensuremath{\mathbb{U}}
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    -
                                                                                                                                                                                                                                                                                                                                                                                                   MEROPS; C14.004;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    entities requires
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 <del>:</del>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  s SWISS-PROT entry is copyright. It is produced through a collaboration ween the Swiss Institute of Bioinformatics and the EMBL outstation - Buropean Bioinformatics Institute. There are no restrictions on its
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            SIMILARITY: BELONGS TO PEPTIDASE FAMILY CAUTION: WHAT WE CALL ALPHA' ISOFORM IS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         SUBJUNITS. PROPERTIDE DOMAINS CAN ALSO BE CLEAVED EFFICIENTLY BY CPP32 PROTEASE. ACTIVE HETERODIMERS BETWEEN THE SMALL SUBUNIT OF CASPASE-7 AND THE LARGE SUBUNIT OF CPP32 PROTEASE ALSO OCCUR AND VICE VERSA
                                                                                                                                                                                                                                                                                                                                                                             601761; -
                                                                                                                                                                                                                                                                                                                                                                                                              P42574;
                                                                                                                                                                                                                                                                                                                                                                                                                         BC015799;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  VERSA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              N: WHAT WE CALL ALPHA' ISOFORM IS KNOWN IN REF.4
BETA IS ALREADY DEFINED IN REF.3 WE HAVE CALLED
                                    194
                                                         186
                                                                                                                                                            24
199
207
144
186
                                                                                                                                                                                                                                                                                                                                                                                                            1PAU.
                                                                                                                                                                                                                                                                                                                                                                                                                                AAC51153.1; -.
AAF21460.1; -.
                         AA;
                                                                                                                                                                                                                                                                                                                                                                                                                         AAH15799.1;
                                                                                                                                                                                                                                       protease;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                statement is not removed. Usage by and for commercial a license agreement (See http://www.isb-sib.ch/announce/
                      186
4
194
34276
                                                                                                                                      303
                                                                                                                                                                    198
206
303
144
186
                                                                                                                                                                                                                                                                                                                                                    ICE_p10
  49.6%;
                                                                                                                                                                                                                                                                                                                                         ICE_p20
                         Ž
                                                                                                                                                                                                                                    Zymogen; Apoptosis; Alternative splicing
                                PSWRSTEKTWKSCRSSPG (IN ISOFORM BETA).
C->A: NO APOPTOTIC ACTIVITY.
D -> E (IN REF. 5).
G -> A (IN REF. 1).
                                                                         (IN ISOFORM ALPHA').

VIYGKDGVTPIKDLTAHFRGDRCKTLLEKPKLFFIQACRGT
ELDDGIQADSGPINDTDANPRYKIPVEADFLFAYSTVPFYY
SWRSPGROSWFVQALCSILEEHGKDLEIMGILTRVUDRVAR
HFESQSDDPHFHEKKQIPCVVSMLTKELYFSQ -> MESCS
VTQAGVQRRDLGRLQPPPPRLAEGPSLMMASRPTRGPSMTQ
MLILDTRSQWKLTSSSPIPRRQAITRGGAQEEAPGLCKPSA
                                                                                                                                                                                CASPASE-7
BY SIMILAR
  Score 725;
                      -> E (IN REF. 5)
-> A (IN REF. 1)
CD373EE54A232CA4
                                                                                                                                                        MDCVGWPPGRKWHLEKNTSCGGSSGICASYVTQM
                                                                                                                                                                                         SUBUNIT
                                                                                                                                                                                                                SUBUNIT
 DB
1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       C14
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Usage
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        its content
                                                                                                                                                                                           P11.
                                                                                                                                                                                                                P20
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           GENERATE THE TWO ACTIVE
Length 303;
                       CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             AS BETA,
IT ALPHA'.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       no no
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       way
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THE REPORT OF A CONTRACT OF A

EMBL; Y13087; HSSP; P42574;

1PAU. CAA73529.1;

(See http://www.isb-sib.ch/announce/

Usage by

and

for

commercia]

MEROPS; C14.005;

MGI:1312921; P42574;

; Casp6. 398; ICE.

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RESULT 9
ICE6_MOUSE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Best Local Similarity 51.: Matches 145; Conservative
by non-profit institutions as long modified and this statement is not removed. entities requires a license agreement '... or send an email to license.
                                                                                                                                                                                                                                                                                                                                                     FEBS Lett. 403:61-69(1997).

-IP FUNCTION: INVOLVED IN THE ACTIVATION CASCADE OF CASPASES
-IP FUNCTION: CLEAVES POLY(ADP-RIBOSE)
POLYMERASE IN VITRO, AS WELL AS LAMINS. OVEREXPRESSION PROMOT
PROGRAMMED CELL DEATH (BY SIMILARITY).
                                                                                                                                                                       -i- PTM: CLEAVAGES BY CPP32, CASPASE-8 OR -10 GE SUBUNITS (BY SIMILARITY).
-i- SIMILARITY: BELONGS TO PEPTIDASE FAMILY C14.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           MEDLINE=97190206; PubMed=9038361; van de Craen M., Vandenabeele P., Devan Loo G., Molemans F., Schotte P.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                01-NOV-1997 (Rel. 35, Created)
01-NOV-1997 (Rel. 35, Last sequence update)
15-JUN-2002 (Rel. 41, Last annotation update)
Caspase-6 precursor (EC 3.4.22.-) (Apoptotic protease Mch-2).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Fiers W.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           STRAIN=C3H/An;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    CASP6
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    008738;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Mus musculus (Mouse)
                                                                                                                                                                                                                                                                                                                                                                                                                                                       *Characterization of seven murine
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    NCBI_TaxID=10090;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ICE6_MOUSE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        259
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           233
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                                                                                                                                                                                                                                                                           SUBCELLULAR LOCATION: Cytoplasmic TISSUE SPECIFICITY: HIGHLY EXPRESS
                                                                                                                                                                                                                                                           TESTIS, AND HEART. LOWER LEVELS
                                                                                                                                                                                                                                                                                                                    SUBUNIT: HETERODIMER OF (BY SIMILARITY).
                                                                                                                SWISS-PROT entry is copyright. It is produced through een the Swiss Institute of Bioinformatics and the Ew
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             MHILTRVNRKVATEFESFSFDATFHAKKQIPCIVSMLTKELYF
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                CVLLSHGEEGIIFGTNGPVDLKKITNFFRGDRCRSLTGKPKLFIIQACRGTELDCGIETD
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  MQILTRVNDRVARHFESQSDDPHFHEKKQIPCVVSMLTKELYF
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           CILLSHGEENVIYGKDGVTPIKDLTAHFRGDRCKTLLEKPKLFFIQACRGTELDDGIQAD
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             HKSTGMTSRSGTDVDAANLRETFRNLKYEVRNKNDLTREEIVELMRDVSKEDHSKRSSFV
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  SGVDDDMAC----HKIPVEADFLYAYSTAPGYYSWRNSKDGSWEIQSLCAMLKQYADKLEF
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         DKYTGMGYRNGTDKDAEALFKCFRSLGFDYIYYNDCSCAKMQDLLKKASEEDHTNAACFA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              SGPINDTDANPRYKIPVEADFLFAYSTVPGYYSWRSPGRGSWFVQALCSILEEHGKDLEI
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    EDSVDAKPDRSSFVPSLFSKKKKNVTMRSIKTTRDRVPTYQYNMNFEKLGKCIIINNKNF
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ENSVDSKSIK-NLEPKIIHGSESMDSGISLDNS----YKMDYPEMGLCIIINNKNF
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    STANDARD;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         51.2%;
                                                                                                                                                                                                                                                                                                                                      A 18
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      PRT;
                                                                                                                                                                                                                                                   EXPRESSED IN LUNG, LIVER, EVELS IN SPLEEN, SKELETAL
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Declercq W., van
P., van Criekinge
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                                                                   There are no rest
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77;
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                                                                                                                                                                                                                    GENERATE THE TWO ACTIVE
                                                                                                                                                                                                                                                                                                                                                                                                                                                       members.";
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                                                                                                                                                                                                                                                                           LIVER, KIDNEY
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                                                                                           restrictions
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Beyaert
                                                                                                                                                                                                                                                         MUSCLE,
                                                                                                                EMBL
                                                                                                                        a collaboration -
MBL outstation -
                                                                                                                                                                                                                                                                                                                                                                           PROMOTES
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  12;
                                                                                                                  outstation
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                                                                                                                                                                                                                                                                                                                                                                      P55212;
01-OCT-1996 (Rel. 34, Created)
01-OCT-1996 (Rel. 34, Last sequence update)
15-JUN-2002 (Rel. 41, Last annotation update)
15-CT-6 precursor (EC 3.4.22.-) (Apoptotic
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       _HUMAN
ICE6_HUMAN
                          Srinivasula S.M., Fernandarmstrong R.C., Wang L., Alnemri E.S.;
                                                                  TISSUE-Lymphocytes;
MEDLINE-97059171; PubMed-8900201;
                                                                                                                                                                                                    MEDLINE=95316841; PubMed=7796396; Fernandes:Alnemri T., Litwack G.,
                                                                                                                                                                           "Mch2, a family.";
                                                                                                                                                                                                                                                                                                                      Eukaryota; Metazoa;
Mammalia; Eutheria;
                                                                                                                      PROCESSING
                                                                                                                                                          Cancer Res.
                                                                                                                                                                                                                                                                                                                                Homo sapiens (Human).

Motazoa; Chordata;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ACT_SITE
                                                                                                                                                                                                                                                  TISSUE-T-cel]
                                                                                                                                                                                                                                                                 SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                     NCBI_TaxID=9606;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        CHAIN
PROPEP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 SEQUENCE
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   PRINTS; PR00376; ILIBCENZYME. SMART; SM00115; CASC; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Pfam; PF00655; Pfam; PF00656;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 InterPro;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             InterPro;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 205
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         Ced-3/interleukin
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  FASMLTKKLHF
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        SWRNSKDGSWFIQSLCAMLKQYADKLEFMHILTRVNRKVATEFESFSFDATFHAKKQIPC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  LFIIQACRGTELDCGIETDSGVD------
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         YKMDYPEMGLCIIINNKNFHKSTGMTSRSGTDVDAANLRETFRNLKYEVRNKNDLTREEI 96
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          IFIIQACRGSQHDVPVVPLDMVDHQTDKLDNVTQVDAASVYTLPAGADFLMCYSVAEGYY
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       VELMRDVSKEDHSKRSSFVCVLLSHGEEGIIFGTNGPVDLKKITNFFRGDRCRSLTGKFK 156
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       YKMDHKRRGVALIFNHERFFWHLTLPERRGTNADRDNLTRRFSDLGFEVKCFNDLRAEEL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       PF00655; ICE_p10; 1.
PF00656; ICE_p20; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Similarity
                                                                                                                                                                                     new member of the apoptotic
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              IPR002138;
IPR001309;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            163
177
104
146
276
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Thiol
                                                                                                                                                  55:2737-2742(1995).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       STANDARD;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 A,
                                                       Fernandes-Alnemri T.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    270
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           protease;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 5
162
176
276
276
104
                                                                                                                                                                                                                                                                                                                     Primates;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        36.0%;
41.4%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               31595
   lbeta converting
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ICE_p20
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             CE_p10
                                        Trapani J.A.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              MW;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     42;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Apoptosis; Zymogen.
BY SIMILARITY.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      CASPASE-6 SUBUNIT P18 (
BY SIMILARITY.
CASPASE-6 SUBUNIT P11 (
BY SIMILARITY.
BY SIMILARITY.
BY SIMILARITY.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Score 526; DB 1;
Pred. No. 4.4e-37;
                                                                                                                                                                                                                                                                                                                     Craniata; Vertebrata; Catarrhini; Hominidae,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Mismatches
                                                                                                                                                                                                      Alnemri E
                                                                                                                                                                                     Ced-3/Ice
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       293
                                    , Zangrilli J., I
   enzyme-like
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              -DDMACHKIPVEADFLYAYSTAPGYY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ₹
                                                                                                                                                                                                                                                                                                                     Hominidae;
                                                                                                                                                                                                                                                                                                                                                                                         protease
                                                                                                                                                                                   cysteine
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Length
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          CRC64
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Indels
                                                                                                                                                                                                                                                                                                                                  Euteleostomi;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             (BY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   (BY
homolog
                                                       Robertson
                                                                                                                                                                                                                                                                                                                                                                                         Mch-2)
                                      Litwack
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       276;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             SIMILARITY)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 SIMILARITY).
                                                                                                                                                                                   protease
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 12;
 Mch6 and
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                                                   Z
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            199
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                139
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       264
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            204
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Best Local
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                                                                                                                                                                                                                                                                                                      PROPEP
CHAIN
ACT_SITE
ACT_SITE
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SEQUENCE
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mediator CPP32.";
J. Biol. Chem. 271:27099-27106(1996).

-i- FUNCTION: INVOLVED IN THE ACTIVATION CASCADE OF CASPASES
RESPONSIBLE FOR APOPTOSIS EXECUTION. CLEAVES POLY(ADP-RIBOSE)
RESPONSIBLE FOR APOPTOSIS EXECUTION. OVEREXPRESSION PROMOTES
                                                                                                                                                                                                                                                                                                                                                                                                                        PROSITE; PS01122; CASPASE_CYS;
PROSITE; PS01121; CASPASE_P10;
PROSITE; PS50207; CASPASE_P20;
PROSITE; PS50208; CASPASE_P20;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Pfam; PF00655; ICE_p10; 1.
Pfam; PF00656; ICE_p20; 1.
PRINTS; PR00376; IL1BCENZYME.
SMART; SM00115; CASC; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           InterPro;
InterPro;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             EMBL; U20536; AAC50168.1;
EMBL; U20537; AAC50169.1;
HSSP; P42574; 1PAU.
MEROPS; C14.005; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             entities requires a license agreement (S or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               This SWISS-PROT entry is copyright. It is produced through between the Swiss Institute of Bioinformatics and the Enthe European Bioinformatics Institute. There are no restant
                                                                                                                                                                                                                                                                                                                                                                                    CHAIN
                                                                                                                                                                                                                                                                                                                                                                                                 Hydrolase;
PROPEP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Genew;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       modified and this statement
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                InterPro;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     MIM; 601532;
                264
                                          217
                                                                   204
                                                                                            157
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                                                                                                                                               97
                                                                                                                                                                        97
                                                                                                                                                                                                 37
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        SUBUNIT: HETERODIMER OF A 18 kDa (P18) SUBCELLULAR LOCATION: CYTOPLASMIC. ALTERNATIVE PRODUCTS: 2 ISOFORMS; ALPH ARE PRODUCED BY ALTERNATIVE SPLICING. SEEM TO HAVE PROTEOLYTIC ACTIVITY. PTM: CLEAVAGES BY CPP32, CASPASE-8 OR
CIVSMLTKELYFY
| |||||:|:|:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 SIMILARITY: BELONGS TO PEPTIDASE FAMILY C14.
                                                           YSWRNSKDGSWFIQSLCAMLKQYADKLEFMHILTRVNRKVATEFESFSFDATFHAKKQIP
                                                                                                        LFIIQACRGTELDCGI------ETDSGVDDDMACHKIPVEADFLYAYSTAPGY
                                                                                                                                          LLKIHEVSTVSHADADCFVCVFLSHGEGNHIYAYDAKIEIQTLTGLFKGDKCHSLVGKPK
                                                                                                                                                                                            YKMDHRRRGIALIFNHERFFWHLTLPERRRTCADRDNLTRRFSDLGFEVKCFNDLKAEEL
                                                                                                                                                                                                           YKMDYPEMGLCIIINNKNFHKSTGMTSRSGTDVDAANLRETFRNLKYEVRNKNDLTREEI 96
                                    YSHRETYNGSWYIQDLCEMLGKYGSSLEFTELLTLYNRKVSQRRVDFCKDPSAIGKKQVP
                                                                                        IFIIQACRGNQHDVPVIPLDVVDNQTEKLDTNITEVDAASVYTLPAGADFLMCYSVAEGY
                                                                                                                                                                 VELMRDVSKEDHSKRSSFVCVLLSHGEEGIIFGTNGPVDLKKITNFFRGDRCRSLTGKPK 156
                                                                                                                                                                                                                                                     104;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 HGNC:1507; CASP6.
                                                                                                                                                                                                                                                              Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            IPR002398; ICE.
IPR002138; ICE_p10
IPR001309; ICE_p20
                                                                                                                                                                                                                                                                                                       293
                                                                                                                                                                                                                                                    Conservative
                                                                                                                                                                                                                                                                                                      Ä
                                                                                                                                                                                                                                                                                                                                                                                              protease;
23
              276
                                                                                                                                                                                                                                                                                                                  179
193
293
121
163
102
                                                                                                                                                                                                                                                            35.4%;
41.1%;
                                                                                                                                                                                                                                                                                                      33409
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ormatics Institute. There are no rest institutions as long as its content
                                                                                                                                                                                                                                                                                                   MW;
                                                                                                                                                                                                                                                    42;
                                                                                                                                                                                                                                                                                                                                                                                                         Apoptosis; Zymogen; Alternative splicing
                                                                                                                                                                                                                                                  Score 517.5;
Pred. No. 2.4e
42; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 is not removed. Usage by and for commerciar agreement (See http://www.isb-sib.ch/announce/
                                                                                                                                                                                                                                                                                                                           CASPASE-6 SUBUNIT P11
BY SIMILARITY.
BY SIMILARITY.
                                                                                                                                                                                                                                                                                                                  MISSING
                                                                                                                                                                                                                                                                                                                                                                                CASPASE-6 SUBUNIT P18
                                                                                                                                                                                                                                                                                                   BD9204E23CE1F670 CRC64;
                                                                                                                                                                                                                                                                                                                  (IN ISOFORM BETA)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ALPHA (SHOWN ING. THE BETA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           OR -10 GENERATE
                                                                                                                                                                                                                                                                .4e-36;
                                                                                                                                                                                                                                                                           DB 1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         A 11 kDa (P11) SUBUNIT
                                                                                                                                                                                                                                                                         Length
                                                                                                                                                                                                                                                  Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     HERE) AND BETA;
ISOFORM DOES NO
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              restrictions
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           THE TWO ACTIVE
                                                                                                                                                                                                                                                                         293;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         EMBL
                                                                                                                                                                                                                                                 13;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           a collaboration
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          outstation
                                                                                                                                                                                                                                                Gaps
                                     276
                                                              263
                                                                                        216
                                                                                                                203
                                                                                                                                          156
                                                                                                                                                                                             96
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   on
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 way
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CFASMLTKKLHFF

DROME

ICE_DROME

STANDARD;

PRT;

339

001382; Q9VAH1; 01-NOV-1997 (Re

)1-NOV-1997 (Rel. 35, 16-OCT-2001 (Rel. 40, 15-JUN-2002 (Rel. 41,

Created)

update)

update)

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RA Abril J.F., Doyle C., Baxter E.G., Heit G., Nelsom C.R., Fielier B.D., RA Abril J.F., Agbayani A., An H.-J., Andrews-Pfannkoch C., Baldwin D., RA Ballew R.M., Basu A., Baxendale J., Bayraktaroglu L., Beasley E.M., RA Beeson K.Y., Benos P.V., Berman B.P., Bhandari D., Bolshakov S., RA Beeson K.Y., Benos P.V., Berman B.P., Bhandari D., Bolshakov S., RA Berson E.K., Davies P., Davies P., Borther A., Chandra I., RA Cherry J.M., Cawley S., Dahlke C., Davenport L.B., Davies P., RA Cherry J.M., Cawley S., Dahlke C., Davenport L.B., Davies P., RA Cherry J.M., Cawley S., Dahlke C., Davenport L.B., Davies P., RA Cherry J.M., Cawley S., Dahlke C., Davenport L.B., Davies P., RA Cherry J.M., Cawley S., Dahlke C., Davenport L.B., Davies P., RA Cherry J.M., Cawley S., Dahlke C., Davenport L.B., Davies P., RA Cherry J.M., Cawley S., Celbert M.M., Glasser K., RA Cherry J., Carrell J.H., Gu Z., Gunn P., Harris M., RA Glodek A., Gong F., Gorrell J.H., Gu Z., Gunn P., Harris M., RA Harris N.L., Harvey D., Heiman T.J., Hernandez J.R., Houck J., RA Hostin D., Houston K.A., Howland T.J., Wei M.-H., Ibegwam C., RA Kimmel B.E., Kodira C.D., Kraft C.K., Kravitz S., Kulp D., Lai Z., Liang Y., Lin X., Mattei B., McIntosh T.C., McLeod M.P., McPherson D. RA Merkulov G., Milshina N.V., Mobarry C., Morris J., Moshrefi A., Nalson D.L., RA Melson D.R., Nelson D.K., Nalson D.L., RA Palazzolo M., Pittman G.S., Pan S., Pollard J., Puri V., Reese M.G., RA Palazzolo M., Pittman G.S., Pan S., Pollard J., Puri V., Reese M.G., RA Allians S.M., Woy M., Murphy B., Murphy L., Muzny D.M., Nelson D.L., RA Palazzolo M., Pittman G.S., Pan S., Pollard J., Puri V., Reese M.G., RA Allians S.M., Woodage T., Wanders R.D.C., Scheeler F., Shen H., Ra Spier E., Spradling A.C., Stapleton M., Skupski M.P., Smith T., Ra Spier E., Spradling A.C., Stapleton M., Skupski M.P., Smith T., Ra Zheng X.H., Wang X., Wang S., Yao O.A., Weinster E., Wang A.H., Wang X., Wang S., Yao O.A., Walson C., Nala M., Zhang G., Zhao O.A., Zheng L., Fall S., 2105 (2000).

CC. The Grant S. M
                      -!- FUNCTION: INVOLVED IN THE ACTIVATION CASCADE
RESPONSIBLE FOR APOPTOSIS EXECUTION. ACTS DOW
CLEAVES BACULOVIRUS P35 AND LAMIN DMO IN VITY
-!- SUBUNIT: HETERODIMER OF A 21 kDa (P21) AND A
-!- DEVELOPMENTAL STAGE: EXPRESSED AT ALL STAGES
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Adams M.D., Celniker S.E., Holt R.A., Evans C.A., Gocayne J.D., Amanatides P.G., Scherer S.E., Li P.W., Hoskins R.A., Galle R.F., George R.A., Lewis S.E., Richards S., Ashburner M., Henderson S.N., Sutton G.G., Wortman J.R., Yandell M.D., Zhang Q., Chen L.X., Sutton G.G., Wortman J.R., Yandell M.D., Zhang Q., Chen L.X., Brandon R.C., Rogers Y.-H.C., Blazej R.G., Champe M., Pfeiffer B.D., Wan K.H., Doyle C., Baxter E.G., Helt G., Nelson C.R., Miklos G.L.G., haril T.F., Acharati A., M. L., T., M. L., M. 
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            MEDLINE=20196006; PubMed=10731132;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            EMBO J. 16:2805-2813(1997).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Fraser A.G.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Muscomorpha; Eph
NCBI_TaxID=7227;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Drosophila melanogaster (Fruit fly).
Eukaryota; Metazoa; Arthropoda; Mandibulata; Pancrustacea; Hexapoda;
Insecta; Pterygota; Neoptera; Endopterygota; Diptera; Brachycera;
Muscomorpha; Ephydroidea; Drosophilidae; Drosophila.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Caspase precursor (EC ICE OR CG7788.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         "Identification of a Drosophila melanogaster ICE/CED-3-related protease, drICE.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    MEDLINE-97327558; PubMed-9184225;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Evan G.I.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Last sequence upda
Last annotation up
3.4.22.-) (drICE)
              P35 AND LAMIN DMO IN VITRO.
OF A 21 kDa (P21) AND A 12 kDa
EXPRESSED AT ALL STAGES WHERE A
                                                                                                                         DOWNSTREAM
                  APOPTOSIS
                                                   (P12) SUBUNIT
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      SOLUTION STATES OF THE STATES 
DICEL_SPOFR
TCEL_SPOFR
STANDARD; PRT; 299 AA.

C P89116;
T 01-NOV-1997 (Rel. 35, Created)
T 01-NOV-1997 (Rel. 35, Last sequence update)
T 11-JUN-2002 (Rel. 41, Last annotation update)
E Caspase-1 precursor (EC 3.4.22.-).
S Spodoptera frugiperda (Fall armyworm).
S Spodoptera frugiperda; Mendibulata; Par C Eukaryota; Metazoa; Arthropoda; Mandibulata; Par C Insecta; Pterygota; Neoptera; Endopterygota; Leg
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Pfam; PF00656; ICE_p20; 1.
PRINTS; PR00376; IL1BCENZYME
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PROSITE; PS50207; CASPASE_P10;
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use by non-profit institutions as long as its content
modified and this statement is not removed. Usage by ar
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Lepidoptera; Glossata;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             SEQUENCE
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Alnemri E.S.;
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NCBI_TaxID=7108;
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FUNCTION: INVOLVED IN THE ACTIVATION CASCADE OF CASPASES RESPONSIBLE FOR APOPTOSIS EXECUTION (BY STMILARITY). INH.
THE BACULOVIRUS ANTI-APOPTOTIC PROTEIN P35. CLEAVES P35.
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2.4e-32;
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RA Adams M.D., Celniker S.E., Holt R.A., How, Hoskins R.A., Galle R.F.,
RA Barndon R.C., Rogers Y.H.C., Blaze's R.G., Champe M., Pfelffer B.D.,
RA Burdon R.C., Rogers Y.H.C., Blaze's R.G., Champe M., Pfelffer B.D.,
RA Ballew R.M., Basu A., Baxendale J., Bayraktaroglu L., Beasley E.M.,
RA Ballew R.M., Basu A., Baxendale J., Bayraktaroglu L., Beasley E.M.,
RA Ballew R.M., Basu A., Baxendale J., Bayraktaroglu L., Beasley E.M.,
RA Beeson K.Y., Benos P.V., Berman B.P., Bhandari D., Bishakov S.,
RA Bortis K.C., Busam D.A., Butler H., Galeu E., Center A., Chandra I.,
RA Bortis K.C., Busam D.A., Butler H., Galeu E., Center A., Chandra I.,
RA Cherry J.M., Cawley S., Dahlke C., Davenport L.B., Davies P.,
RA Dodson K., Doup L.E., Downes M., Dugan-Rocha S., Dunkov B.C., Dunn P.,
RA Dodson K., Doup L.E., Downes M., Dugan-Rocha S., Dunkov B.C., Dunn P.,
RA Glodek A., Gong F., Gorrell J.H., Gu Z., Guan P., Harris M.,
RA Harris N.L., Harvey D., Helman T.J., Hernandez J.R., Houck J.,
RA Harris N.L., Harvey D., Helman T.J., Hernandez J.R., Houck J.,
RA Harris N.L., Mattei B., McIncosh T.C., McLeed M.P., McPherson D.,
RA Kimmel B.E., Kodira C.D., Kraft C., Kravitz S., Kulp D., J.A., Ketchum K.A.,
RA Melson D.R., Nelson K.A., Nixon K., Nusskern D.R., McShrefi A.,
RA Melson D.R., Nusbon K., Nusskern D.R., McShrefi A.,
RA Reinert K., Semidyton K., Saunders R.D.C., Scheeler F., Shen H.,
RA Reinert K., Seminyton K., Saunders R.D.C., Scheeler F., Shen H.,
RA Sylrakas R., Tector C., Turner R., Ventris J., Woshrefi A.,
RA Harris N., Woodage T., Worley R., Smith T.,
RA Sylrakas R., Tector C., Turner R., Ventra J.S., Zhao W., Yang S., Yao Q.A.,
The Global R., Shen H., Shina M., Zhang G., Zhao Q., A.,
Then J., Shinh H.O.,
The Global R., Northey S., Shinh M., Shon K., Shen H.,
Schen S., Zhao M., Stong G., Shoo Q., Zheng L.,
Then J., Shinh H.O.,
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Science 275:536-540(1997).
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Insecta; Pterygota; Neoptera; Endopterygota; Diptera; Brachycera;
Muscomorpha; Ephydroidea; Drosophilidae; Drosophila.
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FUNCTION: INVOLVED IN THE ACTIVATION CASCADE OF CASPASES RESPONSIBLE FOR APOPTOSIS EXECUTION (BY SIMILARITY). PROTEDLYTICALLY CLEAVES POLY(ADP.RIBOSE) POLYMERASE (PARP). OF ZYGOTIC DCP-1 FUNCTION CAUSES LARVAL LETHALITY AND MELANC
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PROSITE; PS01121; CASPASE_HIS; 1
PROSITE; PS50207; CASPASE_P10; 1
PROSITE; PS50208; CASPASE_P20; 1
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MEROPS; C14. ....
FlyBase; FBgn0010501;
FlyBase; FBgn002398; ICE.
InterPro; IPR002138; ICE_P10.
InterPro; IPR001309; ICE_P20.
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ICE_P10; 1.
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Q14790; Q14791;
Q15806; Q9UQ81;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           use by non-profit institutions as long as its content modified and this statement is not removed. Usage by an entitles requires a license agreement (See http://www.isb-or send an email to license@isb-sib.ch).
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SUBUNIT: HETERODIMER OF A 22 kDa (P22) AND A 13 kDa (P13) SUBUNIT: SUBUNIT: HETERODIMER OF A 22 kDa (P22) AND A 13 kDa (P13) SUBUNIT: DEVELOPMENTAL STAGE: PRESENT UNIFORMLY THROUGHOUT EMBRYOS OF STAGES 4 AND 10. IN STAGE 16 EMBRYOS, THE EXPRESSION BECOMES RESTRICTED TO THE CENTRAL NERVOUS SYSTEM, THE DEVELOPING GONADS, AND A PORTION OF THE GUT. IN STAGE 17 EMBRYOS, EXPRESSION IS MAINLY LOCALIZED IN CELLS ALONG THE MIDLINE OF THE CENTRAL NERVO
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               European Bioinformatics Institute. There
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                                                                                                            DGSWFIQSLCAMLKQYADKLEFMHILTRVNRKVATEFESFSFDAT--FHAKKQIPCIVSM:|||:|| | :|||:||
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                                                                                                                                                                       DILKHVGKAAELDHTDNDCLAVAILSHGEHGYLYAKDTQYKLDNIWHYFTATFCPSLAGK
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BY SIMILARITY.
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           Q14794; Q14795; Q14796; Q15780;
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SEQUENCE FROM N.A. (ISOFORM 2-ALPHA).
MEDLINE-97373543; PubMed-9228018;
Srinivasula S.M., Ahmad M., Ottilie S., Bullr
Fernandes-Alnemri T., Croce C.M., Litwack G.,
Armstrong R.C., Alnemri E.S.;
"FLAME-1, a novel FADD-like anti-apoptotic mo
Fas/TNFR1-induced apoptosis.";
J. Biol. Chem. 272:18542-18545(1997).
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MEDLINE=96353838; PubMed=8755496;

Fernandes-Alnemri T., Armstrong R.C., Krebs J., Srini
Wang L., Bullrich F., Fritz L.C., Trapani J.A., Tomas
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                                                                                                                                      protease Mch5 is a CrmA-inhibitable protease that a Ced-3/ICE-like cysteine proteases."; Proc. Natl. Acad. Sci. U.S.A. 93:14486-14491(1996).
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          MEDLINE=99132295; PubMed=9931493; Grenet J., Teitz T., Wei T., Valentine "Structure and chromosome localization Gene 226:225-232(1999).
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zymogens
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Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                01-NOV-1997 (Rel. 35, Created)
01-NOV-1997 (Rel. 35, Last sequence update)
15-JUN-2002 (Rel. 41, Last annotation update)
15-JUN-2002 (Rel. 41, Last annotation update)
Caspase-8 precursor (EC 3.4.22-) (ICE-like apoptotic protease 5)
(MORT1-associated CED-3 homolog) (MACH) (FADD-homologous ICE/CED-3-like protease) (FADD-like ICE) (FLICE) (Apoptotic cysteine protease)
                                                                                                                                                                                                                   'Molecular ordering
                                                                                                                                                                                                                                                                                                                                          9
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       SEQUENCE FROM N.A., AND PARTIAL MEDLINE=96279827; PubMed=8681377
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           TISSUE=Thymus, and B-cell; MEDLINE=96279826; PubMed=8681376;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             (Apoptotic protease Mch-5) (CAP4). CASP8 OR MCH5.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Cell 85:803-815(1996).
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               NCBI_TaxID=9606;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             SEQUENCE FROM N.A.,
       induced
                                                                                                                                                                                                                of the Fas-apoptotic
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               AND
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                                                                                                                                                                                                                                                             Fernandes-Alnemri
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                of,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     b-3-like protease,
signaling complex
                 system. Cleavage of
                                                                                                                                                                                                                                                                                                                                                                                                                                                  Bullrich F., ck G., Tomase
                                                                                                                                                                                     pathway:
ease that
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             O'Rourke Gentz R.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   the
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Kidd V.J.
the human
                                                                                                                                                                                                                                                                                                                                                                                                        molecule
                                                                                                                                                                                                                                                             Τ.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                       Tomaselli
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Tomaselli K.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             R.,
                                                                                                                                                                                     the Fas/APO-1 activates multiple
                                                                                                                                                                                                                                                             Litwack
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  novel
                                                                                                                                                                                                                                                                                                                                                                                                      that regulates
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           CASP8 gene
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Mann
                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Banks
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            protease,
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nn M.,
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                                                                                                                                                                                                                                                                                                                                                                                                                                                       K. J
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                 caspase
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PROCESSING. MEDLINE=97327557;

8

Biol.

Chem.

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EMBL;
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EMBL;
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                                                                                                                                                                                                                                                                                                           EMBL;
EMBL;
                                                                                                                                                                                                                                                                                                                                                                                  EMBL;
EMBL;
EMBL;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                use by non-profit institutions as long a modified and this statement is not removed. entities requires a license agreement (See I
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   This SWISS-PROT entry is copyright. It is produced through between the Swiss Institute of Bioinformatics and the Exthe European Bioinformatics Institute. There are no restricted the European Bioinformatics Institute.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        signaling complex (DISC).";
EMBO J. 16:2794-2804(1997).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      or send
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Structure 7:1125-1133(1999)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 "The three-dimensional structure of caspase-8:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Krammer P.H.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Medema J.P., Scaffidi C., Kischkel F.C., Shevchenko A., Mann M. Krammer P.H., Peter M.E.;
"FLICE is activated by association with the CD95 death-inducing
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  PTM: GENERATION OF THE SUBUNITS REQUIRES ASSOCIATION WITH THE DISC, WHEREAS ADDITIONAL PROCESSING IS LIKELY DUE TO THE AUTOCATALYTIC ACTIVITY OF THE ACTIVATED PROTEASE, GRANZYME B CASPASE-10 CAN BE INVOLVED IN THESE PROCESSING EVENTS.
SIMILARITY: BELONGS TO PEPTIDASE FAMILY C14.
SIMILARITY: CONTAINS 2 DEATH EFFECTOR DOMAINS (DED).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ALTERNATIVE PRODUCTS: 8 ISOFORMS; 1-ALPHA (SHOWN HERE), 2-ALPHA/MCH5-BETA, 3-ALPHA, 4-ALPHA, 1-BETA, 2-BETA, 3-BETA AND 4-BETA, 3-RETA AND ATTERNATIVE SPLICING.
TISSUE SPECIFICITY: ALPHA 1 AND BETA 1 ISOFORMS ARE EXPRESSED IN WIDE VARIETY OF TISSUES. HIGHEST EXPRESSION IN PERIPHERAL BLOOD LEUKOCYTES, SPLEEN, THYMUS, AND LIVER. BARELY DETECTABLE IN BRAIN TESTIS, AND SKELETAL MUSCLE.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          SUBUNIT: HETERODIMER OF A 18 kDa
                                                                                                                                                                                                                                                                                                                                                                             X98172; CAA66853.1; -. X98173; CAA66854.1; -. X98174; CAA66855.1; -. X98175; CAA66856.1; -. X98176; CAA66857.1; -. X98178; CAA66859.1; -. X98178; -. X981
w; HGNC:1509;
601763; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     INTERACTS WITH CFLAR.
                                                                       1QDU;
                                                                                            AF102146;
AF102139;
AF102140;
AF102141;
AF102142;
AF102143;
AF102143;
AF102145;
AF009620;
                                                                                                                                                                                                                                                                                                                                                             U58143;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   CRYSTALLOGRAPHY (2.8 ANGSTROMS).
                                                                                                                                                                                                                                                                                                                                  U60520;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Tomaselli K.J.,
                                                                                                                                                                                                                                                                                                                                AAC50602.1;
AAC50645.1;
                                                                                         AAD24962.1; JOINED
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Gruetter M.G.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     INHIBITORY PROTEIN.
8 kDa (P18) AND A 10 kDa (P10)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              (See http://www.isb-sib.ch/announce/
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                as its content
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                EMBL
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     a collaboration
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           for
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IN BRAIN,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                outstation
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 J.F.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      commercial
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RESULT 15
ICE9_HUMAN STANDARD; PRT; 41/
ID ICE9_HUMAN STANDARD; PRT; 41/
AC P55211; Q92852; O95348; Q9UIJ8; Q9UEQ3;
DT 01-OCT-1996 (Rel. 34, Created)
                                                                           Db
                                                                                           QY
                                                                                                             Ъ
                                                                                                                               Qγ
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Best Local S
Matches 102
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       InterPro; IPR001875; DED.
InterPro; IPR002138; ICE_p10.
InterPro; IPR001309; ICE_p20.
Pfam; PF00655; ICE_p10; 1.
Pfam; PF00656; ICE_p20; 1.
Pfam; PF01335; DED; 2.
                                                                                                                                                                                                                                                                                                          CONFLICT
CONFLICT
                                                                                                                                                                                                                                                                                                                                                                 VARSPLIC
VARSPLIC
VARSPLIC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  PROPEP
CHAIN
ACT_SITE
ACT_SITE
                                                                                                                                                                                                                                                                                                                                                                                                                VARSPLIC
VARSPLIC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Repeat;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    PROSITE;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       PROSITE; PROSITE;
                                                                                                                                                                                                                                                                                                  SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                      VARSPLIC
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DOMAIN
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        CHAIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Hydrolase; Thiol
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           PROSITE; PS50168; DED;
                                                                           453
                                                                                                                                                   333
                                                                                           246
                                                                                                              393
                                                                                                                                187
                                                                                                                                                                     136
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                                                                                                                                                                                                                           217
                                                                                                                                                                                                         77
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                                                                           X---
                                                                                                                                                TFRNLKYEVRNKNDLTREEIVELMRDVSKEDHSKRSSFVCVLLSHGEEGIIFGTNG-PVD
                                                                                                                                                                                                                                          SESMDSGISLDNSYKMDYPEMGLCIIINNKNFHKST-----GMTSRSGTDVDAANLRE
                                                                                                                                                                    LKKITNFFRGDRCRSLTGKPKLFIIQACRGTELDCGI--ETDSG----VDDDMACHK---
                                                                                                                                                                                      TFEELHFEIKPHDDCTVEQIYEILKIYQLMDHSNMDCFICCILSHGDKGIIYGTDGQEAP
                                                                                                                                                                                                                          SESQ----TLDKVYQMKSKPRGYCLIINNHNFAKAREKVPKLHSIRDRNGTHLDAGALTT
                                                                                                                                                                                                                                                              102;
                                                                                                             EFESFSFDATFHAKKQIPCIVSMLTKELYF
                                                                                                                                IPVEADFLYAYSTAPGYYSWRNSKDGSWFIQSLCAMLKQYADK-LEFMHILTRVNRKVAT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ; 3D-structure.

1 216

217 374

217 384

375 384

385 479

317 317

317 317
                                                                                                                                                                                                                                                                       Similarity
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PS01121;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     PS50208;
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                                                                                                                                                                                                                                                                                                 285
294
331
479
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199
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375
385
317
360
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236
269
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                                                                                                                                                                                                                                                               Conservative
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                                                                                                                                                                                                                                                                                                  AA;
                                                                                                                                                                                                                                                                                          285
294
331
55391
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  protease;
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; CASPASE_HIS;
; CASPASE_P10;
; CASPASE_P20;
                                                                                                                                                                                                                                                                                                                                                                   479
479
276
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80
177
                                                                                                                                                                                                                                                                                                                                                 479
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235
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                                                                                                                                                                                                                                                                                                                                                                                                                                                     220
                                                                                                                                                                                                                                                                       28.8%;
                                                                                                                                                                                                                                                                                                   ¥.
                                                                                                                                                                                                                                                               49;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Apoptosis;
                                                                                                                                                                                                                                                                      Score 421; L
                                                                                                                                                                                                                                                                                                            D -> H
E -> D
-> P
                                                                                                                                                                                                                                                                                                                                                                           MISSING
                                                                                                                                                                                                                                                              Pred. No. 5.70
); Mismatches
                                                                                                                                                                                                                                                                                                                                       BETA)
                                                                                                                                                                                                                                                                                                                                                                                               \begin{array}{lll} {\tt DFGQSLPNEKQTSGILSDHQQSQFCKSTGESAQTSQH} \\ {\tt ISOFORM} & 1 & {\tt BETA} \end{array} ) \; . \\ \\ \end{array} 
                                                                                                                                                                                                                                                                                                                                                                                                                GEELCGVMTISDSPREQDSESQTLDKVYQMKSKPRGY
                                                                                                                                                                                                                                                                                                                                                                                                                                                    ALPHA AND ISOFORM 4 BETA). ERSSSLEGSPDEFSNGEELCGVMTISDSPREQDSESQ
                                                                                                                                                                                                                                                                                                                                               MISSING (IN ISOFORM 3 BETA AND ISOFORM
                                                                                                                                                                                                                                                                                                                                                                                                                          MISSING (IN ISOFORM 3 ALPHA)
                                                                                                                                                                                                                                                                                                                                                                                                                                           DFGQSLPNEKQTSGILSDHQQSQFCKSTGESAQTSQH
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        CASPASE-8
                                                                                                                                                                                                                                                                                                                                                         AND ISOFORM
                                                                                                                                                                                                                                                                                                                                                                                                                                                                     (IN ISOFORM 4 ALPHA)
MISSING (IN ISOFORM
                                                                                                                                                                                                                                                                                                   7A5FEAA6B39B582F
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        RFHFCRMSWAEANSQCQTQSVPFWRRVDHLLIR
                                                                                           275
                                                                                                                                                                                                                                                                                                           (IN REF. 3 AND 5).
(IN REF. 4).
(IN REF. 2 AND 4).
                                                                                                                                                                                                                                                                                                                                                                          (IN ISOFORM 2 BETA)
(IN ISOFORM 1 BETA)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Zymogen; Alternative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        SUBUNIT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       SUBUNIT
                                                                                                                                                                                                                                                                       DB 1;
.7e-28;
                                                                                                                                                                                                                                                                                                                                                          4 BETA)
                                                                                                                                                                                                                                                                                                                                                                 FGNVFSWW (IN ISOFORM
                                                                                                                                                                                                                                                                                                                                                                                                                                                             4 ALPHA).
                                                                                                                                                                                                                                                              91;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      P10
                                                                                                                                                                                                                                                                                                 CRC64;
                                                                                                                                                                                                                                                                               Length 479;
                                                                                                                                                                                                                                                               Indels
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SEQUENCE FROM N.A.
MEDLINE-96279246; PubMed-8663294;
MEDLU Orth K., Chinnaiyan A.M.,
                                                                                                                                                                                                                              Miho Y.,
"A novel
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                MEDLINE=99315341; PubMed=10384055; Hadano S., Nasir J., Nichol K., Rasper D.M., Vaillancourt J.P. Sherer S.W., Beatty B.G., Ikeda J.E., Nicholson D.W., Hayden M. "Genomic organization of the human caspase-9 gene on chromoson 1p36.1-p36.3.";
                                                                                                                                                Seol
                                                                                                                                                          SEQUENCE FROM N.A. (SHORT ISOFORM). MEDLINE=99107856; PubMed=9890966;
                                                                                                                                                                                                                                                                                     Izawa M., Mori T.; Ito H., Sairenji T.;

"Molecular cloning and sequencing of a cDNA predicting an alternative form of pro-caspase-9 from human castric cancer cell lines.";
Submitted (JUN-1998) to the EMBL/GenBank/DDBJ databases.
                                                                                                                                                                                                                                                                                                                                                                                "Identification of an endogenous dominant-negative short isoform caspase-9 that can regulate apoptosis."; cancer Res. 59:999-1002(1999).
                                                                                                                                                                                                                                                                                                                                                                                                                             MEDLINE=99168502; PubMed=10070954; Srinivasula S.M., Ahmad M., Guo Y., Fernandes-Alnemri T., Alnemri E.S.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                the lamin-cleaving enzyme Mch2alpha mediator CPP32.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Caspase-9 precursor (EC 3.4.22.-) (CASP-9) (ICE-like apoptotic protease 6) (ICE-LAP6) (Apoptotic protease Mch-6) (Apoptotic protease activating factor 3) (APAF-3).
                                                                                                                                                                                                                    activity
                                                                                                                                                                                                                                                     SEQUENCE FROM N.A. (SHORT ISOFORM).
                                                                                                                                                                                                                                                                                                                                                TISSUE-Stomach
                                                                                                                                                                                                                                                                                                                                                                                                                                                                          SEQUENCE FROM N.A. (SHORT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Alnemri
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Srinivasula
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          SEQUENCE FROM N.A.,
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                                                                                                                                                                                                                                                                                                                                Izawa M., Mori T., Ito
                                                                                                                                                                                                                                                                                                                                                           SEQUENCE FROM N.A.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Eukaryota; Metazoa; Chordata; Mammalia; Eutheria; Primates;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             CASP9 OR MCH6
                                                                                                                 nhibitor
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        "The Ced-3/interleukin 1beta
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    "ICE-LAP6,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Homo sapiens (Human).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    NCBI_TaxID=9606;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              16-OCT-2001 (Rel. 40, 15-JUN-2002 (Rel. 41,
                                 ol D.W., Billiar T.K.;

caspase-9 variant missing the catalytic site is an endogenous hibitor of apoptosis.";

Biol. Chem. 274:2072-2076(1999).

- FUNCTION: INVOLVED IN THE ACTIVATION CASCADE OF CASPASES RESPONSIBLE FOR APOPTOSIS EXECUTION. BINDING OF CASPASE-9 TO PROPEOSIBLE FOR APOPTOSIS EXECUTION. BINDING OF CASPASE AND 1 LEADS TO ACTIVATION OF THE PROTEASE WHICH THEN CLEAVES AND 1 LEADS TO ACTIVATION OF THE PROTEOSIBLE FOR POLY(ADP-RIBOSE)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Biol. Chem.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Biol.
              ACTIVATES CASPASE-3. PROTEOLYTICALLY POLYMERASE (PARP). FUNCTION: THE SHORT ISOFORM LACKS ACT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      the cytotoxic
     INHIBITOR OF CASPASE-9
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Genome 10:757-760(1999).
                                                                                                                                                                                                                     splicing product
                                                                                                                                                                                                                                                Momoi
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Chem. 271:16720-16724(1996).
                                                                                                                                                                                                 (DEC-1998) to the EMBL/GenBank/DDBJ databases
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   R.C., Wang
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 a novel member of the ICE/Ced-3 otoxic T cell protease granzyme
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   S.M.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             271:27099-27106(1996)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Fernandes-Alnemri T.,
ang L., Trapani J.A.,
                                                                                                                                                                                                                                                                                                                                                           (SHORT ISOFORM)
                                                                                                                                                                                                                                             Fujita
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           AND PROCESSING
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Last sequence update
                                                                                                                                                                                                                           of human caspase-9 lacking protease
                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ISOFORM).
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Craniata; Vertebrata; Euteleostomi; Catarrhini; Hominidae; Homo.
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                 ACTIVITY
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B.";
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                                                                                                                                                                                                                                                                                                                                                                                                                                          Lazebnik
                SI
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                ΑN
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                DOMINANT-NEGATIVE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             chromosome
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N
                                                                       APAF-
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SEQUENCE
              CONFLICT
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SUBUNIT: Heterodimer

of a 35 kDa (P35) and a

10

kDa (P10) subunit

8

46195 Œ.

874E90F17F8DC4CD

CRC64;

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CONFLICT
CONFLICT
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                                                                               ACT_SITE
ACT_SITE
VARSPLIC
                                                                                                                       CHAIN
                                                                                                                                                                             Hydrolase; PROPEP
                                                                                                                                                                                                                                 PROSITE; PS50209; CARD; 1.
PROSITE; PS01122; CASPASE_CYS;
PROSITE; PS01121; CASPASE_HIS;
                                                                                                                                                                                                                                                                                                                  Pfam; PF00619; CARD; 1.
Pfam; PF00655; ICE_p10; 1.
Pfam; PF00656; ICE_p20; 1.
                                                                                                                                                                                                                                                                                                                                                           InterPro;
InterPro;
                                                                                                                                                                                                                PROSITE; PS01121; CASPASE_HIS; PROSITE; PS50207; CASPASE_P10;
                                                                                                                                                                                                                                                                                        SMART;
                                                                                                                                                                                                                                                                                                                                                                                                                  MIM;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     EMBL;
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                                                                                                                                                   PROPEP
                                                                                                                                                                                                          PROSITE; PS50208;
                                                                                                                                                                                                                                                                              SMART;
                                                                                                                                                                                                                                                                                                     PRINTS; PR00376;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
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                                                                                                                                                                                                                                                                                                                                                                                      InterPro;
                                                                                                                                                                                                                                                                                                                                                                                                 InterPro;
                                                                                                                                                                                                                                                                                                                                                                                                                               Genew;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             between
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               s SWISS-PROT entry is copyright. It is produced through a ween the Swiss Institute of Bioinformatics and the EMBL Buropean Bioinformatics Institute. There are no restrict by non-profit institutions as long as its content is
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                PIM: CLEAVAGES AT ASP-315 BY GRANZYME B AND GENERATE THE TWO ACTIVE SUBUNITS. CASPASE-8 INVOLVED IN THESE PROCESSING EVENTS.
SIMILARITY: BELONGS TO PEPTIDASE FAMILY C14.
SIMILARITY: CONTAINS 1 CARD DOMAIN.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 terminal CED-3 homologous domains in and AFP. Interacts with BIRC7.
ALTERNATIVE PRODUCTS: 2 ISOFORMS; A LIBERE AND A SHORT/9S/BETA FORM; ARE PEDICTUS SPECIFICITY: UBIQUITOUS, WITH HEART, MODERATE EXPRESSION IN LIVER,
                                                                                                                                                                                                                                                                                                                                                                                                                 602234;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          PANCREAS.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Caspase-9 and APAF1 bind to each other via their respective NH2 terminal CED-3 homologous domains in the presence of cytochrome
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    M60521; AA
AB019197;
AB019199;
AB019199;
AB019200;
AB019200;
AB019201;
AB0192023;
AB019204;
AB01920999;
                                                                                                                                                                                                                                                                                                                                                                                                                                                          P42574;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 U56390;
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                                                                                                                                                                                                                                                                          SM00114; CARD;
SM00115; CASC;
                                                                                                                                                                                                                                                                                                                                                                                                                              HGNC:1511;
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IPR002138; ICE_p10.
IPR001309; ICE_p20.
                                                                                                                                                                                                                                                                                                                                                                                                 IPR001315; CARD.
237
287
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36
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                                                                                                                                                                                            Thiol
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AAC50776.1;
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BAA82697.1;
BAA82697.1;
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BAA82697.
AAD12248.
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BAA82697.
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BAA82697.
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BAA87905.1;
                                                                                                                                                                                                                                                                                                       IL1BCENZYME
                                                                                                                                                                                           protease;
                                                                                                                                                                                                      CASPASE_P20;
                                                                                                                                                                                                                                                                                                                                                                                                                              CASP9
                          315
330
416
426
92
237
287
289
289
289
32
32
                                                                                                                                                                                        Zymogen;
         BY SIMILARITY.
BY SIMILARITY:
MISSING (IN SHORT I
A -> V (IN REF. 1 A
S -> R (IN REF. 1).
A -> G (IN REF. 1).
D -> L (IN REF. 1).
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                                                                                                                        CARD
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                                                                                                                                     SUBUNIT
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AND 7).
4, 5 AND
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                                                                                                                                                                                           Alternative
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Ouery Match 28.0%; Score 410; DB 1; Length 416; Best Local Similarity 32.8%; Pred. No. 4e-27; Matches 90; Conservative 51; Mismatches 91; Indels 42; Gaps 34 DNSYKMDYPEMGLCIIINNKNFHKSTGMTSRSGTDVDAANLRETFRNLKYEVRNKNDLTR 93 1;
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Search completed: December 2, 2002, 12:56:30 Job time: 10.5517 secs